STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 151908

TO: Dave Nguyen **Location: rem/2d31/2c18** **Art Unit: 1632** **Friday, April 29, 2005** **Case Serial Number: 10/068160**	**From: Toby Port** **Location: Biotech-Chem Library** **REM1-A59** **Phone: 272-2523** **toby.port@uspto.gov**

Search Notes

Dear Examiner Nguyen,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 791.351 Seconds
(without alignments)
1224.620 Million cell updates/sec

Title: US-10-068-160A-1
Perfect score: 20
Sequence: 1 ggtgcatcgatgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AX194432	AX194432 Sequence
2	20	100.0	20	6	AX194434	AX194434 Sequence
3	20	100.0	20	6	AX194437	AX194437 Sequence
4	20	100.0	20	6	AX194438	AX194438 Sequence
5	20	100.0	20	6	AX194443	AX194443 Sequence
6	20	100.0	20	6	AX194472	AX194472 Sequence
7	20	100.0	20	6	AX352198	AX352198 Sequence
8	20	100.0	20	6	AX352209	AX352209 Sequence
9	20	100.0	20	6	AX352242	AX352242 Sequence
10	20	100.0	20	6	AX465382	AX465382 Sequence
11	20	100.0	20	6	AX465384	AX465384 Sequence
12	20	100.0	20	6	AX465387	AX465387 Sequence
13	20	100.0	20	6	AX465388	AX465388 Sequence
14	20	100.0	20	6	AX465393	AX465393 Sequence
15	20	100.0	20	6	AX465422	AX465422 Sequence
16	20	100.0	20	6	AX816067	AX816067 Sequence
17	20	100.0	22	6	AX352204	AX352204 Sequence
18	20	100.0	22	6	AX352248	AX352248 Sequence
19	20	100.0	28	6	AX352219	AX352219 Sequence
20	20	100.0	28	6	AX352231	AX352231 Sequence
21	20	100.0	29	6	AX352237	AX352237 Sequence
22	20	100.0	30	6	AX352225	AX352225 Sequence
23	20	100.0	30	6	AX352230	AX352230 Sequence
24	20	100.0	32	6	AX352167	AX352167 Sequence
25	19	95.0	19	6	AX194453	AX194453 Sequence
26	19	95.0	19	6	AX194473	AX194473 Sequence
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28	19	95.0	19	6	AX465423	AX465423 Sequence
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33	18.4	92.0	20	6	AX194501	AX194501 Sequence
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35	18.4	92.0	20	6	AX194506	AX194506 Sequence
36	18.4	92.0	20	6	AX194507	AX194507 Sequence
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ALIGNMENTS

RESULT 1
AX194432
LOCUS AX194432 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 32 from Patent WO0151500.
ACCESSION AX194432
VERSION AX194432.1 GI:15385088
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 32 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
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Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 2
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LOCUS AX194434 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 34 from Patent WO0151500.
ACCESSION AX194434
VERSION AX194434.1 GI:15385090
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 34 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 3
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LOCUS       AX194437                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 37 from Patent WO0151500.
ACCESSION   AX194437
VERSION     AX194437.1  GI:15385093
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 37 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 4
AX194438
LOCUS       AX194438                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 38 from Patent WO0151500.
ACCESSION   AX194438
VERSION     AX194438.1  GI:15385094
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 38 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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ORIGIN

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RESULT 5
AX194443
LOCUS       AX194443                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 43 from Patent WO0151500.
ACCESSION   AX194443
VERSION     AX194443.1  GI:15385099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 43 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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ORIGIN

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              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 6
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LOCUS       AX194472                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 72 from Patent WO0151500.
ACCESSION   AX194472
VERSION     AX194472.1  GI:15385128
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 72 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 GGTGCATCGATGCAGGGGGG 20
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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 7
AX352198
LOCUS       AX352198                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 494 from Patent WO0193902.
ACCESSION   AX352198
VERSION     AX352198.1  GI:18617481
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 494 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
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ORIGIN

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Qy          1 GGTGCATCGATGCAGGGGGG 20
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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 8
AX352209
LOCUS       AX352209                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 505 from Patent WO0193902.
ACCESSION   AX352209
VERSION     AX352209.1  GI:18617492
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 505 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 18;
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Qy          1 GGTGCATCGATGCAGGGGGG 20
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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 9
AX352242
LOCUS       AX352242                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 538 from Patent WO0193902.
ACCESSION   AX352242
VERSION     AX352242.1  GI:18617525
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 538 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 18;
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RESULT 10
AX465382
LOCUS       AX465382                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 50 from Patent WO0211761.
ACCESSION   AX465382
VERSION     AX465382.1  GI:21899745
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 50 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 11
AX465384
LOCUS       AX465384                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 52 from Patent WO0211761.
ACCESSION   AX465384
VERSION     AX465384.1  GI:21899747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
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  JOURNAL   Patent: WO 0211761-A 52 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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RESULT 12
AX465387
LOCUS       AX465387                 20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 55 from Patent WO0211761.
ACCESSION   AX465387
VERSION     AX465387.1  GI:21899750
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 55 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 13
AX465388
LOCUS       AX465388                 20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 56 from Patent WO0211761.
ACCESSION   AX465388
VERSION     AX465388.1  GI:21899751
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 56 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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RESULT 14
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DEFINITION  Sequence 61 from Patent WO0211761.
ACCESSION   AX465393
VERSION     AX465393.1  GI:21899756
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 61 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 GGTGCATCGATGCAGGGGGG 20


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DEFINITION  Sequence 90 from Patent WO0211761.
ACCESSION   AX465422
VERSION     AX465422.1  GI:21899785
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 90 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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Job time : 791.476 secs

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 203.919 Seconds
(without alignments)
580.598 Million cell updates/sec

Title: US-10-068-160A-1
Perfect score: 20
Sequence: 1 ggtgcatcgatgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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5	20	100.0	20	4	AAC80618	Aac80618 Immunogen
6	20	100.0	20	4	AAC80623	Aac80623 Immunogen
7	20	100.0	20	4	AAS09622	Aas09622 Immunorea
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11	20	100.0	20	4	AAS09584	Aas09584 Immunorea
12	20	100.0	20	4	AAS09588	Aas09588 Immunorea
13	20	100.0	20	6	ABL35568	Abl35568 Immunosti
14	20	100.0	20	6	ABL35579	Abl35579 Immunosti
15	20	100.0	20	6	ABL35612	Abl35612 Immunosti
16	20	100.0	20	6	ABK46500	Abk46500 Immunosti
17	20	100.0	20	6	ABK46460	Abk46460 Immunosti
18	20	100.0	20	6	ABK46465	Abk46465 Immunosti
19	20	100.0	20	6	ABK46471	Abk46471 Immunosti
20	20	100.0	20	6	ABK46462	Abk46462 Immunosti
21	20	100.0	20	6	ABK46466	Abk46466 Immunosti
22	20	100.0	20	8	ACC48309	Acc48309 CpG oligo
23	20	100.0	20	8	ACC48295	Acc48295 CpG oligo
24	20	100.0	20	8	ACC48310	Acc48310 CpG oligo
25	20	100.0	20	8	ACC48316	Acc48316 CpG oligo
26	20	100.0	20	9	ACC83150	Acc83150 D class O
27	20	100.0	20	9	ACC83115	Acc83115 D class C
28	20	100.0	20	9	ACC83151	Acc83151 D class O
29	20	100.0	20	9	ACC83114	Acc83114 D class C
30	20	100.0	20	9	ACC83121	Acc83121 D class C
31	20	100.0	20	10	ADB84186	Adb84186 CpG conta
32	20	100.0	20	10	ADC51789	Adc51789 D19 SEQ I
33	20	100.0	20	10	ADD01074	Add01074 CpG D oli
34	20	100.0	20	10	ADD01048	Add01048 CpG D oli
35	20	100.0	20	12	ADK67597	Adk67597 Immunosti
36	20	100.0	20	12	ADN97043	Adn97043 Immunosti
37	20	100.0	20	12	ADN97042	Adn97042 Immunosti
38	20	100.0	20	12	ADP83754	Adp83754 Immunosti
39	20	100.0	20	12	ADP83753	Adp83753 Immunosti
40	20	100.0	20	13	ADQ16875	Adq16875 Immunomod
41	20	100.0	22	6	ABL35574	Abl35574 Immunosti
42	20	100.0	22	6	ABL35618	Abl35618 Immunosti
43	20	100.0	28	6	ABL35601	Abl35601 Immunosti
44	20	100.0	28	6	ABL35589	Abl35589 Immunosti
45	20	100.0	29	6	ABL35607	Abl35607 Immunosti

ALIGNMENTS

RESULT 1
AAC80652
ID AAC80652 standard; DNA; 20 BP.
XX
AC AAC80652;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:72.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX

PS Claim 4; Page 35; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20
```

RESULT 2
AAC80614
ID AAC80614 standard; DNA; 20 BP.
XX
AC AAC80614;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:34.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 29; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20
```

RESULT 3

```
AAC80612
ID   AAC80612 standard; DNA; 20 BP.
XX
AC   AAC80612;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:32.
XX
KW   CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW   immunogenic; cytokine release; natural killer cell; NK cell activation;
KW   cell-mediated immune response; T-cell response; humoral response;
KW   B-cell response; antibody production; immune response induction; vaccine;
KW   allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW   parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW   rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW   immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW   antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW   antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200061151-A2.
XX
PD   19-OCT-2000.
XX
PF   12-APR-2000; 2000WO-US009839.
XX
PR   12-APR-1999;   99US-0128898P.
XX
PA   (KLIN/) KLINMAN D.
PA   (ISHI/) ISHII K.
PA   (VERT/) VERTHELYI D.
XX
PI   Klinman D,  Ishii K,  Verthelyi D;
XX
DR   WPI; 2001-006880/01.
XX
PT   Novel oligonucleotides useful for the prevention and treatment of
PT   allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT   resulting from exposure to a bio-warfare agent.
XX
PS   Claim 4; Page 29; 46pp; English.
XX
CC   The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC   (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC   comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC   -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC   optionally have phosphorothioate linkages which make them more resistant
CC   to degradation. The invention also relates to an oligonucleotide delivery
CC   complex comprising an oligonucleotide of the invention and a targetting
CC   agent, and a pharmaceutical composition comprising the oligonucleotide
CC   delivery complex. The oligonucleotides are able to induce either a cell-
CC   mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC   oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC   cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC   being able to induce a humoral response. It is thought that after
CC   administration, the oligonucleotide acts on antigen-presenting cells
CC   (e.g., macrophages and dendritic cells), which then release cytokines,
CC   leading to activation of natural killer (NK) cells. A cell-mediated or
CC   humoral response can then occur by activation of T- or B-cells. The
CC   induction of an immune response is useful for treating, preventing or
CC   ameliorating an allergic reaction (preferably asthma), or an infection,
CC   where an immunogenic CpG oligonucleotide is administered either alone or
CC   in combination with an anti-allergenic agent or anti-infectious agent.
CC   The allergic conditions which may be treated include eczema, allergic
CC   rhinitis, hayfever, urticaria, food allergies and other atopic
CC   conditions, and the infections which may be treated include viral,
CC   bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC   leishmania and schistosomiasis. Immune response induction may also be
CC   used in the treatment of an autoimmune disorder (e.g., lupus
CC   erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC   associated with immune system deficiency, and symptoms resulting from
CC   exposure to an agent of biological warfare. An immunogenic CpG
CC   oligonucleotide, either alone or in combination with an anti-cancer
CC   agent, is useful for treating solid tumour cancer. The induction of an
CC   immune response is used in antisense therapy and to improve the efficacy
CC   of a vaccine. The oligonucleotide is preferably administered to
CC   lymphocytes ex vivo, producing activated lymphocytes which are then
CC   administered to the host. The present sequence represents an immunogenic
CC   CpG oligodeoxynucleotide of the invention
XX
SQ   Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 4
AAC80617
ID   AAC80617 standard; DNA; 20 BP.
XX
AC   AAC80617;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:37.
XX
KW   CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW   immunogenic; cytokine release; natural killer cell; NK cell activation;
KW   cell-mediated immune response; T-cell response; humoral response;
KW   B-cell response; antibody production; immune response induction; vaccine;
KW   allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW   parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW   rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW   immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW   antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW   antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200061151-A2.
XX
PD   19-OCT-2000.
XX
PF   12-APR-2000; 2000WO-US009839.
XX
PR   12-APR-1999;   99US-0128898P.
XX
PA   (KLIN/) KLINMAN D.
PA   (ISHI/) ISHII K.
PA   (VERT/) VERTHELYI D.
XX
PI   Klinman D,  Ishii K,  Verthelyi D;
XX
DR   WPI; 2001-006880/01.
XX
PT   Novel oligonucleotides useful for the prevention and treatment of
PT   allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT   resulting from exposure to a bio-warfare agent.
XX
PS   Claim 4; Page 29; 46pp; English.
XX
CC   The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC   (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC   comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC   -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC   optionally have phosphorothioate linkages which make them more resistant
CC   to degradation. The invention also relates to an oligonucleotide delivery
CC   complex comprising an oligonucleotide of the invention and a targetting
CC   agent, and a pharmaceutical composition comprising the oligonucleotide
```

CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 5
AAC80618
ID AAC80618 standard; DNA; 20 BP.
XX
AC AAC80618;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:38.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 6
AAC80623
ID AAC80623 standard; DNA; 20 BP.
XX
AC AAC80623;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:43.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 7
AAS09622
ID AAS09622 standard; DNA; 20 BP.
XX
AC AAS09622;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #72.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 39; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,

CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 8
AAS09582
ID AAS09582 standard; DNA; 20 BP.
XX
AC AAS09582;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #32.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 32; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 9
AAS09587
ID AAS09587 standard; DNA; 20 BP.
XX
AC AAS09587;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #37.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 33; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection

CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 10
AAS09593
ID AAS09593 standard; DNA; 20 BP.
XX
AC AAS09593;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #43.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 34; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 11
AAS09584
ID AAS09584 standard; DNA; 20 BP.
XX
AC AAS09584;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #34.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 32; 48pp; English.
XX

```
CC   AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC   nucleotides comprising multiple CpG sequences, where one of the CpG
CC   sequences is different from another of the multiple CpG sequences. The
CC   ODN are useful for inducing an immune response, preferably a cell-
CC   mediated immune response, involving non-B cell activation, interferon
CC   gamma (IFN-gamma) production or a humoral immune response involving B
CC   cell activation, antibody and interleukin-6 production in a host, for
CC   treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC   cancer, e.g. solid tumour cancer, a disease associated with the immune
CC   system e.g. autoimmune disorder or an immune system deficiency, infection
CC   or a symptom resulting from exposure to bio-warfare agent in a human. The
CC   induction of immune response improves the efficacy of a vaccine and is
CC   used in antisense therapy. The ODN are useful for treating, preventing or
CC   ameliorating allergic reactions, including eczema, allergic rhinitis or
CC   coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC   and other atopic conditions, for improving the efficacy of vaccines
CC   against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC   malaria, for treating immune system deficiencies, e.g. lupus
CC   erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC   multiple sclerosis, infections including Francisella, schistosomiasis,
CC   tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC   symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC   Anthrax and Listeria
XX
SQ   Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 12
AAS09588
ID   AAS09588 standard; DNA; 20 BP.
XX
AC   AAS09588;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Immunoreactive CpG sequence-containing oligonucleotide #38.
XX
KW   CpG sequence; immune response; non-B cell activation; interferon gamma;
KW   IFN-gamma; humoral; antibody production; interleukin-6 production;
KW   therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW   bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW   coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW   hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW   lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW   schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW   Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS   Synthetic.
XX
PN   WO200151500-A1.
XX
PD   19-JUL-2001.
XX
PF   12-JAN-2001; 2001WO-US001122.
XX
PR   14-JAN-2000; 2000US-0176115P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman D,  Ishii K,  Verthelyi D;
XX
DR   WPI; 2001-442129/47.
XX
PT   Oligodeoxynucleotides for inducing an immune response to treat and
PT   prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT   resulting from exposure to bio-warfare agents, comprise multiple CpG
PT   sequences.
XX
PS   Claim 5; Page 33; 48pp; English.
XX
CC   AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC   nucleotides comprising multiple CpG sequences, where one of the CpG
CC   sequences is different from another of the multiple CpG sequences. The
CC   ODN are useful for inducing an immune response, preferably a cell-
CC   mediated immune response, involving non-B cell activation, interferon
CC   gamma (IFN-gamma) production or a humoral immune response involving B
CC   cell activation, antibody and interleukin-6 production in a host, for
CC   treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC   cancer, e.g. solid tumour cancer, a disease associated with the immune
CC   system e.g. autoimmune disorder or an immune system deficiency, infection
CC   or a symptom resulting from exposure to bio-warfare agent in a human. The
CC   induction of immune response improves the efficacy of a vaccine and is
CC   used in antisense therapy. The ODN are useful for treating, preventing or
CC   ameliorating allergic reactions, including eczema, allergic rhinitis or
CC   coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC   and other atopic conditions, for improving the efficacy of vaccines
CC   against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC   malaria, for treating immune system deficiencies, e.g. lupus
CC   erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC   multiple sclerosis, infections including Francisella, schistosomiasis,
CC   tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC   symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC   Anthrax and Listeria
XX
SQ   Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 13
ABL35568
ID   ABL35568 standard; DNA; 20 BP.
XX
AC   ABL35568;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 494.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
```

PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Klinman DM;
XX
DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 61; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 14
ABL35579
ID ABL35579 standard; DNA; 20 BP.
XX
AC ABL35579;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 505.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .20
FT /*tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
PN WO200193902-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018276.
XX
PR 07-JUN-2000; 2000US-0209797P.
XX
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Klinman DM;
XX
DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 61; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 15
ABL35612
ID ABL35612 standard; DNA; 20 BP.
XX
AC ABL35612;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 538.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .20
FT /*tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
PN WO200193902-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018276.
XX
PR 07-JUN-2000; 2000US-0209797P.
XX
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Klinman DM;
XX

DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 61; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGTGCATCGATGCAGGGGGG 20
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Db          1 GGTGCATCGATGCAGGGGGG 20
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Search completed: April 29, 2005, 06:25:59
Job time : 206.919 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1875.14 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-1
Perfect score: 20
Sequence: 1 ggtgcatcgatgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18.4	92.0	257	1	AV268287	AV268287 AV268287
2	17.4	87.0	240	1	AV281636	AV281636 AV281636
3	17.4	87.0	303	1	AV269637	AV269637 AV269637
c 4	17.4	87.0	473	4	BI507147	BI507147 BB170025B
c 5	17.4	87.0	1214	5	BQ898390	BQ898390 AGENCOURT
c 6	17	85.0	541	8	B01614	B01614 cSRL-134g10
c 7	17	85.0	807	6	CA101677	CA101677 SCACHR104
c 8	17	85.0	839	9	CG066914	CG066914 PUIBJ87TD
c 9	16.8	84.0	272	5	BX639713	BX639713 BX639713
10	16.8	84.0	597	1	AV028453	AV028453 AV028453
c 11	16.8	84.0	631	4	BJ244833	BJ244833 BJ244833
12	16.8	84.0	638	1	AL692509	AL692509 AL692509
c 13	16.8	84.0	648	6	CB065500	CB065500 EST645181
c 14	16.8	84.0	655	7	CO101616	CO101616 GR__Eb002
15	16.8	84.0	671	4	BJ229325	BJ229325 BJ229325
c 16	16.8	84.0	671	6	CA920724	CA920724 EST638442
17	16.8	84.0	685	4	BJ634520	BJ634520 BJ634520
18	16.8	84.0	697	4	BJ250701	BJ250701 BJ250701
c 19	16.8	84.0	740	4	BJ617983	BJ617983 BJ617983
20	16.8	84.0	868	9	CG675673	CG675673 trs3405 t
21	16.8	84.0	927	4	BI733127	BI733127 603354541
c 22	16.8	84.0	979	6	CA157988	CA157988 SCEZRZ304
c 23	16.8	84.0	1206	9	CG747404	CG747404 P040-4-H0
c 24	16.4	82.0	245	2	AW325275	AW325275 TENU4637
c 25	16.4	82.0	259	2	BB422123	BB422123 BB422123
c 26	16.4	82.0	277	8	AQ444154	AQ444154 GSSTc0207
27	16.4	82.0	374	6	CB966250	CB966250 NL34_G07
c 28	16.4	82.0	553	8	BH374854	BH374854 AG-ND-105
29	16.4	82.0	584	5	BQ875411	BQ875411 QGI8A19.y
c 30	16.4	82.0	621	8	BH450526	BH450526 BOGFX73TR
c 31	16.4	82.0	665	7	CO075430	CO075430 GR__Ea36C
32	16.4	82.0	670	8	BH996954	BH996954 oep83h09.
c 33	16.4	82.0	679	8	BH577346	BH577346 BOGGD05TR
c 34	16.4	82.0	700	8	BH685253	BH685253 BOMMA43TR
c 35	16.4	82.0	702	8	BH471235	BH471235 BOGRT27TR
c 36	16.4	82.0	705	9	CE730492	CE730492 tigr-gss-
37	16.4	82.0	712	5	BQ860936	BQ860936 QGC17B11.
c 38	16.4	82.0	738	8	BZ063097	BZ063097 lld86b12.
c 39	16.4	82.0	747	8	BZ449138	BZ449138 BONHP21TF
40	16.4	82.0	815	6	CA766588	CA766588 AF53-Rpf_
c 41	16.4	82.0	853	8	BZ449800	BZ449800 BONDQ35TR
c 42	16.4	82.0	866	8	BH128747	BH128747 G-3o11 Ma
c 43	16.4	82.0	915	9	CC588288	CC588288 CH240_386
c 44	16.4	82.0	960	9	AG073881	AG073881 Pan trogl
c 45	16.4	82.0	1014	9	AG056417	AG056417 Pan trogl

ALIGNMENTS

RESULT 1
AV268287
LOCUS AV268287 257 bp mRNA linear EST 05-NOV-1999
DEFINITION AV268287 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930534F16 3', mRNA sequence.
ACCESSION AV268287
VERSION AV268287.1 GI:6256324
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 257)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for

further details.
FEATURES Location/Qualifiers
source 1. .257
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930534F16"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis (DH10B)"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

Query Match 92.0%; Score 18.4; DB 1; Length 257;
Best Local Similarity 95.0%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||.|||||||||
Db 95 GGTGCATCGAGGCAGGGGGG 114

RESULT 2
AV281636
LOCUS AV281636 240 bp mRNA linear EST 05-NOV-1999
DEFINITION AV281636 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933425J05 3', mRNA sequence.
ACCESSION AV281636
VERSION AV281636.1 GI:6269673
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 240)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .240
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933425J05"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis (DH10B)"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 240;
Best Local Similarity 94.7%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGCATCGATGCAGGGGGG 20
|||||||||.|||||||||
Db 84 GTGCATCGAGGCAGGGGGG 102

RESULT 3
AV269637
LOCUS AV269637 303 bp mRNA linear EST 05-NOV-1999
DEFINITION AV269637 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930544G09 3', mRNA sequence.
ACCESSION AV269637
VERSION AV269637.1 GI:6257674
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 303)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .303
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930544G09"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis (DH10B)"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 303;
Best Local Similarity 94.7%; Pred. No. 6.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGCATCGATGCAGGGGGG 20
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Db 142 GTGCATCGAGGCAGGGGGG 160

RESULT 4
BI507147/c

LOCUS BI507147 473 bp mRNA linear EST 08-APR-2002
DEFINITION BB170025B20H07.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170025B20H07 5', mRNA sequence.
ACCESSION BI507147
VERSION BI507147.1 GI:15357521
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 473)
AUTHORS Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
JOURNAL Genome Res. 12 (4), 555-566 (2002)
MEDLINE 21929762
PUBMED 11932240
COMMENT Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
REPEAT IN THE SEQUENCE
Simple_repeat STRAND (+) ELEMENT (A)n LOCATION [449,468].
PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Plate: BB170025B20 row: H column: 07
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 473.
FEATURES Location/Qualifiers
source 1. .473
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/mol_type="mRNA"
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/db_xref="taxon:7460"
/clone="BB170025B20H07"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
ORIGIN

Query Match 87.0%; Score 17.4; DB 4; Length 473;
Best Local Similarity 94.7%; Pred. No. 6.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGG 19
||||||||| |||||||||
Db 336 GGTGCATCGAAGCAGGGGG 318

RESULT 5
BQ898390/c

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LOCUS       BQ898390               1214 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8712137 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295181
            5', mRNA sequence.
ACCESSION   BQ898390
VERSION     BQ898390.1  GI:22290404
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2501  row: a  column: 06
            High quality sequence stop: 150.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6295181"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 5;  Length 1214;
  Best Local Similarity   94.7%;  Pred. No. 6.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGG 19
              |||||| ||||||||||||
Db        301 GGTGCACCGATGCAGGGGG 283


RESULT 6
B01614/c
LOCUS       B01614                 541 bp    DNA     linear   GSS 13-JUL-1996
DEFINITION  cSRL-134g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo
            sapiens genomic clone cSRL-134g10, genomic survey sequence.
ACCESSION   B01614
VERSION     B01614.1  GI:1410892
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M.,
            Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S. .,
            Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M.,
            Kupfer,K. and Garner,H.R.
  TITLE     Genomic Sequence Sampled Map of Chromosome 11
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Evans GA, Shane Probst
            McDermott Center for Human Growth and Development
            University of Texas Southwestern Medical Center At Dallas
            5323 Harry Hines Blvd, Dallas TX 75235-8591
            Tel: 214-648-1600
            Fax: 214-648-1666
            Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
            PCR PRimers
            FORWARD: TACTAAAGCGAAGCTAGGTG
            BACKWARD: TTTGGACAGATTTAGCTCAG
            Seq primer: T7
            Class: cosmid ends
            High quality sequence stop: 541.
FEATURES             Location/Qualifiers
     source          1. .541
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="cSRL-134g10"
                     /sex="female"
                     /cell_type="chimeric hamster somatic cell hybrid"
                     /clone_lib="cSRL flow sorted Chromosome 11 specific
                     cosmid"
                     /note="Vector: sCos-1; Human Chromosome 11 specific cosmid
                     library prepared from flow sorted human  Chromosome 11
                     derived from Chinese Hampster Ovary (CHO) monochromosomal
                     somatic cell hybrid, J1"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 8;  Length 541;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGG 17
              |||||||||||||||||
Db        181 GGTGCATCGATGCAGGG 165


RESULT 7
CA101677/c
LOCUS       CA101677               807 bp    mRNA    linear   EST 23-SEP-2003
DEFINITION  SCACHR1040C03.g HR1 Saccharum officinarum cDNA clone SCACHR1040C03
            5', mRNA sequence.
ACCESSION   CA101677
VERSION     CA101677.1  GI:34954984
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE   1  (bases 1 to 807)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 040  row: C  column: 03
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .807
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCACHR1040C03"
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/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirilum rubrisubalbicans; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Herbaspirilum rubrisubalbicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Query Match 85.0%; Score 17; DB 6; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCATCGATGCAGGGGGG 20
||||||||||||||||||
Db 32 GCATCGATGCAGGGGGG 16

RESULT 8
CG066914/c
LOCUS CG066914 839 bp DNA linear GSS 19-AUG-2003
DEFINITION PUIBJ87TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0544P06, genomic survey sequence.
ACCESSION CG066914
VERSION CG066914.1 GI:33939094
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 839)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUIBJ87TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .839
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0544P06"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high CoT selected genomic DNA library"
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 839;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTGCATCGATGCAGGGG 18
||||||||||||||||||
Db 124 GTGCATCGATGCAGGGG 108

RESULT 9
BX639713/c
LOCUS BX639713 272 bp mRNA linear EST 12-AUG-2003
DEFINITION BX639713 pBluescript Lion Mus musculus cDNA clone LIONp462H0719 3', mRNA sequence.
ACCESSION BX639713
VERSION BX639713.1 GI:33619588
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 272)
AUTHORS Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schlueter,T., Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Mouse ArrayTAG cDNA (LION)
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONp462H0719.
RZPDLIB;
Mouse ArrayTAG cDNA (LION)
http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=462 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: RP: CAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1. .272
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="LIONp462H0719"
/lab_host="DH10B"
/clone_lib="pBluescript Lion"
ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 272;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||| |||| |||||||||
Db 168 GGTGCCTCGAGGCAGGGGGG 149

RESULT 10
AV028453
LOCUS AV028453 597 bp mRNA linear EST 31-AUG-1999
DEFINITION AV028453 Mus musculus adult C57BL/6J brain Mus musculus cDNA clone 1432000G13, mRNA sequence.
ACCESSION AV028453
VERSION AV028453.1 GI:4783418
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,

```
            Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .597
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="1432000G13"
                     /sex="male"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /clone_lib="Mus musculus adult C57BL/6J brain"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 1;  Length 597;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||||| |||||| ||||
Db         64 GGTGCATCCATGCAGTGGGG 83


RESULT 11
BJ244833/c
LOCUS       BJ244833                631 bp    mRNA    linear   EST 05-APR-2002
DEFINITION  BJ244833 Y. Ogihara unpublished cDNA library, Wh_f Triticum
            aestivum cDNA clone whf16m07 5', mRNA sequence.
ACCESSION   BJ244833
VERSION     BJ244833.1  GI:20057113
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Ogihara,Y. and Murai,K.
  TITLE     Expressed genes in Triticum aestivum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .631
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="whf16m07"
                     /tissue_type="spike at flowering date"
                     /dev_stage="Feekes' scale 10.5.1"
                     /clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 4;  Length 631;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||||| |||||| ||||
Db        559 GGTGCATCGGAGCAGGGGGG 540


RESULT 12
AL692509
LOCUS       AL692509                638 bp    mRNA    linear   EST 21-MAR-2002
DEFINITION  AL692509 NAH Anopheles gambiae cDNA clone NAH-P05-H-10-5, mRNA
            sequence.
ACCESSION   AL692509
VERSION     AL692509.1  GI:19612418
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.
            and Kafatos,F.C.
  TITLE     Anopheles gambiae EST, European Molecular Biology Laboratory
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Christophides GK
            Fotis C. Kafatos laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany
            Tel: +49 6221 387-440
            Fax: +49 6221 387-306
            Email: christop@embl-heidelberg.de
            Plate: P05 row: H column: 10.
FEATURES             Location/Qualifiers
     source          1. .638
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7165"
                     /clone="NAH-P05-H-10-5"
                     /lab_host="E. coli DH10B"
                     /clone_lib="NAH"
                     /note="Vector: pT7T3D-Pac (Pharmacia); Site_1: NotI;
                     Site_2: EcoRI; ESTs sequenced from the T7 priming site
                     that reads from the 5' end of cDNA. The NAP1 is a
                     directionally cloned and normalized, oligo-T primed cDNA
                     library constructed from heads of Anopheles gambiae
                     according to: Bonaldo, Lennon & Soares (1996):
                     Normalization and Subtraction: Two Approaches To
                     Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 1;  Length 638;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||| |||||||||||| |
Db        212 GGTGCAACGATGCAGGGGAG 231


RESULT 13
CB065500/c
LOCUS       CB065500                648 bp    mRNA    linear   EST 21-JAN-2003
DEFINITION  EST645181 HOGA Medicago truncatula cDNA clone HOGA-19K1, mRNA
            sequence.
ACCESSION   CB065500
VERSION     CB065500.1  GI:27811078
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
```

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  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
            Utterback,T., Cho,J. and Fraser,C.M.
  TITLE     ESTs from roots of Medicago truncatula treated with
            oligogalacturonides of DP 6-20
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Michael G. Hahn
            Complex Carbohydrate Research Center
            University of Georgia
            220 Riverbend Road, Athens, GA 30602-4712, USA
            Tel: 706-542-4457
            Fax: 706-542-4412
            Email: hahn@ccrc.uga.edu
            TIGR sequence name: MTMCU61TV
            More information is available at: www.medicago.org
            Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
FEATURES             Location/Qualifiers
     source          1. .648
                     /organism="Medicago truncatula"
                     /mol_type="mRNA"
                     /cultivar="A17"
                     /db_xref="taxon:3880"
                     /clone="HOGA-19K1"
                     /tissue_type="3 day old seedling roots"
                     /dev_stage="24 hours after treatment in the dark at 26 C
                     with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
                     presence of 100 ug/ml Gentamicin"
                     /lab_host="XLOLR"
                     /clone_lib="HOGA"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
                     was directionally ligated into the Unizap XR vector from
                     Stratagene and packaged using Gigapack III Gold packaging
                     extracts. Plasmids containing cDNA inserts were excised
                     from the recombinant lambda-Zap phage using Ex-assist
                     helper phage and propagated in SOLR cells."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 6;  Length 648;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||||||  |||||  ||||
Db        445 GGTGCATCGTTGCAGTGGGG 426


RESULT 14
CO101616/c
LOCUS       CO101616                655 bp    mRNA    linear   EST 16-JUN-2004
DEFINITION  GR__Eb0028C17.f GR__Eb Gossypium raimondii cDNA clone GR__Eb0028C17
            5', mRNA sequence.
ACCESSION   CO101616
VERSION     CO101616.1  GI:48800302
KEYWORDS    EST.
SOURCE      Gossypium raimondii
  ORGANISM  Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 655)
  AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
  TITLE     Global assembly of Cotton ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            Plate: 0028  row: C  column: 17.
FEATURES             Location/Qualifiers
     source          1. .655
                     /organism="Gossypium raimondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:29730"
                     /clone="GR__Eb0028C17"
                     /tissue_type="floral"
                     /dev_stage="-3 to +3 DPA"
                     /lab_host="DH10B"
                     /clone_lib="GR__Eb"
                     /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
                     EcoRV; Library made by Invitrogen with RNA supplied by
                     Wendle lab. Directional cloned into NotI-EV. Colonies
                     plated/picked by AGI. More glycerol clones held in -80."
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 7;  Length 655;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              | ||||||||||  |||||||
Db        200 GATGCATCGATGTAGGGGGG 181


RESULT 15
BJ229325
LOCUS       BJ229325                671 bp    mRNA    linear   EST 05-APR-2002
DEFINITION  BJ229325 Y. Ogihara unpublished cDNA library, Wh_dL Triticum
            aestivum cDNA clone whdl19e17 3', mRNA sequence.
ACCESSION   BJ229325
VERSION     BJ229325.1  GI:20048595
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 671)
  AUTHORS   Ogihara,Y. and Murai,K.
  TITLE     Expressed genes in Triticum aestivum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .671
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="whdl19e17"
                     /tissue_type="crown of seedling"
                     /dev_stage="Feekes' scale 1"
                     /clone_lib="Y. Ogihara unpublished cDNA library, Wh_dL"
ORIGIN

  Query Match             84.0%;  Score 16.8;  DB 4;  Length 671;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||||||  |||||||||
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Db 345 GGTGCATCGGAGCAGGGGGG 364

Search completed: April 29, 2005, 11:55:09
Job time : 1881.14 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 58.5135 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-1
Perfect score: 20
Sequence: 1 ggtgcatcgatgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15.8	79.0	288	4	US-09-270-767-26956	Sequence 26956, A
2		15.8	79.0	2255	4	US-09-270-767-11388	Sequence 11388, A
3		15.8	79.0	3358	3	US-09-248-571-2	Sequence 2, Appli
4		15.8	79.0	3358	3	US-09-553-736-2	Sequence 2, Appli
5		15.8	79.0	66175	4	US-09-949-016-12293	Sequence 12293, A
6	c	15.4	77.0	300598	4	US-09-949-016-11868	Sequence 11868, A
7	c	15.4	77.0	302604	4	US-09-949-016-14588	Sequence 14588, A
8	c	15.4	77.0	302604	4	US-09-949-016-14589	Sequence 14589, A
9	c	15.4	77.0	308362	4	US-09-949-016-17119	Sequence 17119, A
10	c	15.2	76.0	239	4	US-09-513-999C-3027	Sequence 3027, Ap
11	c	15.2	76.0	239	4	US-09-471-276-582	Sequence 582, App
12	c	15.2	76.0	1584	4	US-09-252-991A-7138	Sequence 7138, Ap
13	c	15.2	76.0	1794	4	US-09-252-991A-7259	Sequence 7259, Ap
14		15.2	76.0	1872	4	US-09-252-991A-7359	Sequence 7359, Ap
15		15.2	76.0	47199	4	US-09-949-016-12144	Sequence 12144, A
16		15.2	76.0	47200	4	US-09-949-016-13526	Sequence 13526, A
17	c	15.2	76.0	131631	4	US-09-949-016-11757	Sequence 11757, A
18	c	14.8	74.0	192	4	US-09-270-767-27410	Sequence 27410, A
19	c	14.8	74.0	601	4	US-09-949-016-82180	Sequence 82180, A
20	c	14.8	74.0	601	4	US-09-949-016-82181	Sequence 82181, A
21	c	14.8	74.0	601	4	US-09-949-016-82182	Sequence 82182, A
22	c	14.8	74.0	601	4	US-09-949-016-205054	Sequence 205054,
23	c	14.8	74.0	601	4	US-09-949-016-205055	Sequence 205055,
24	c	14.8	74.0	601	4	US-09-949-016-205056	Sequence 205056,
25		14.8	74.0	622	3	US-09-129-030-46	Sequence 46, Appl
26	c	14.8	74.0	765	4	US-09-270-767-11774	Sequence 11774, A
27		14.8	74.0	9230	4	US-09-949-016-12635	Sequence 12635, A
28		14.8	74.0	9231	4	US-09-949-016-12987	Sequence 12987, A
29	c	14.8	74.0	17032	4	US-09-949-016-12476	Sequence 12476, A
30	c	14.8	74.0	17032	4	US-09-949-016-13352	Sequence 13352, A
31		14.8	74.0	37004	4	US-09-949-016-15317	Sequence 15317, A
32		14.8	74.0	47347	4	US-09-949-016-14130	Sequence 14130, A
33		14.8	74.0	49721	4	US-09-949-016-17538	Sequence 17538, A
34		14.8	74.0	119801	4	US-09-949-016-13453	Sequence 13453, A
35		14.4	72.0	736	4	US-09-270-767-14521	Sequence 14521, A
36	c	14.4	72.0	759	4	US-09-252-991A-1486	Sequence 1486, Ap
37	c	14.4	72.0	1086	4	US-09-252-991A-13644	Sequence 13644, A
38	c	14.4	72.0	1092	4	US-09-252-991A-13444	Sequence 13444, A
39		14.4	72.0	1194	4	US-09-252-991A-13697	Sequence 13697, A
40		14.4	72.0	1308	4	US-09-252-991A-1592	Sequence 1592, Ap
41	c	14.4	72.0	1356	4	US-09-252-991A-1425	Sequence 1425, Ap
42		14.4	72.0	3591	4	US-09-252-991A-1690	Sequence 1690, Ap
43	c	14.4	72.0	4280	4	US-09-079-592-1	Sequence 1, Appli
44	c	14.4	72.0	5496	3	US-09-462-284-1	Sequence 1, Appli
45	c	14.4	72.0	26104	4	US-09-949-016-14045	Sequence 14045, A

ALIGNMENTS

RESULT 1
US-09-270-767-26956
; Sequence 26956, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26956
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26956

Query Match 79.0%; Score 15.8; DB 4; Length 288;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GGTGCATCGATGCAGGGGG 19
              ||||||||| ||||| |||
Db        110 GGTGCATCGGTGCAGTGGG 128
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RESULT 2
US-09-270-767-11388
; Sequence 11388, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11388
; LENGTH: 2255
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11388

Query Match 79.0%; Score 15.8; DB 4; Length 2255;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GGTGCATCGATGCAGGGGG 19
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```
                    ||||||||| ||||| |||
Db        110 GGTGCATCGGTGCAGTGGG 128


RESULT 3
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
;  APPLICANT: BASBAUM, CAROL
;  APPLICANT: GALLUP, MARIANNE
;  APPLICANT: DAIZONG, LI
;  APPLICANT: GEBREMICHAEL, ASSEFA
;  APPLICANT: GENSCH, ERIN
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
;  TITLE OF INVENTION: GENE EXPRESSION
;  FILE REFERENCE: UCSF12/02
;  CURRENT APPLICATION NUMBER: US/09/248,571
;  CURRENT FILING DATE: 1999-02-11
;  EARLIER APPLICATION NUMBER: 60/074,398
;  EARLIER FILING DATE: 1998-02-11
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 3358
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-248-571-2

  Query Match             79.0%;  Score 15.8;  DB 3;  Length 3358;
  Best Local Similarity   89.5%;  Pred. No. 2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTGCATCGATGCAGGGGGG 20
              ||||| | ||||||||||
Db        998 GTGCACCCATGCAGGGGGG 1016


RESULT 4
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
;  APPLICANT:  BASBAUM, Carol
;  APPLICANT:  GALLUP, Marianne
;  APPLICANT:  DAIZONG, Li
;  APPLICANT:  GEBREMICHAEL, Assefa
;  APPLICANT:  GENSCH, Erin
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
;  TITLE OF INVENTION:  MUCIN GENE EXPRESSION
;  FILE REFERENCE:  UCSF-012/03US
;  CURRENT APPLICATION NUMBER: US/09/553,736
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER:  US 09/248,571
;  PRIOR FILING DATE:  1999-02-11
;  PRIOR APPLICATION NUMBER:  US 60/074,398
;  PRIOR FILING DATE:  1998-02-11
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3358
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-553-736-2

  Query Match             79.0%;  Score 15.8;  DB 3;  Length 3358;
  Best Local Similarity   89.5%;  Pred. No. 2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTGCATCGATGCAGGGGGG 20
              ||||| | ||||||||||
Db        998 GTGCACCCATGCAGGGGGG 1016


RESULT 5
US-09-949-016-12293
; Sequence 12293, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12293
;   LENGTH: 66175
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(66175)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12293

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 66175;
  Best Local Similarity   89.5%;  Pred. No. 2.7e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGG 19
              ||| |||| ||||||||||
Db      26863 GGTTCATCCATGCAGGGGG 26881


RESULT 6
US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11868
;   LENGTH: 300598
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(300598)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

  Query Match             77.0%;  Score 15.4;  DB 4;  Length 300598;
  Best Local Similarity   94.1%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TGCATCGATGCAGGGGG 19
```

```
                  ||||| ||||||||||
Db      218203 TGCATAGATGCAGGGGG 218187


RESULT 7
US-09-949-016-14588/c
; Sequence 14588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14588
;   LENGTH: 302604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(302604)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588

  Query Match             77.0%;  Score 15.4;  DB 4;  Length 302604;
  Best Local Similarity   94.1%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TGCATCGATGCAGGGGG 19
              ||||| ||||||||||
Db     268209 TGCATAGATGCAGGGGG 268193


RESULT 8
US-09-949-016-14589/c
; Sequence 14589, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14589
;   LENGTH: 302604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(302604)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

  Query Match             77.0%;  Score 15.4;  DB 4;  Length 302604;
  Best Local Similarity   94.1%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TGCATCGATGCAGGGGG 19
              ||||| ||||||||||
Db     268209 TGCATAGATGCAGGGGG 268193


RESULT 9
US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17119
;   LENGTH: 308362
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(308362)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

  Query Match             77.0%;  Score 15.4;  DB 4;  Length 308362;
  Best Local Similarity   94.1%;  Pred. No. 4.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TGCATCGATGCAGGGGG 19
              ||||| ||||||||||
Db     268025 TGCATAGATGCAGGGGG 268009


RESULT 10
US-09-513-999C-3027/c
; Sequence 3027, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 3027
;   LENGTH: 239
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 23..238
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 22
;   OTHER INFORMATION: s=g or c
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```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 130
;   OTHER INFORMATION: r=a or g
US-09-513-999C-3027

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 239;
  Best Local Similarity   85.0%;  Pred. No. 3.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||||||||  | |  ||||
Db         99 GGTGCATCGATCCTGTGGGG 80


RESULT 11
US-09-471-276-582/c
; Sequence 582, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Duclert A.
;  APPLICANT: Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
;  FILE REFERENCE: GENSET.025CP1
;  CURRENT APPLICATION NUMBER: US/09/471,276
;  CURRENT FILING DATE: 1999-12-21
;  EARLIER APPLICATION NUMBER: 09/057,719
;  EARLIER FILING DATE: 1998-04-09
;  EARLIER APPLICATION NUMBER: 09/069,047
;  EARLIER FILING DATE: 1998-04-28
;  EARLIER APPLICATION NUMBER: PCT/IB99/00712
;  EARLIER FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 1622
;  SOFTWARE: Patent.pm
; SEQ ID NO 582
;   LENGTH: 239
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 159..239
;   NAME/KEY: sig_peptide
;   LOCATION: 159..218
;   OTHER INFORMATION: Von Heijne matrix
;   OTHER INFORMATION: score 4.09999990463257
;   OTHER INFORMATION: seq TVGCAGLAGSCRG/IS
US-09-471-276-582

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 239;
  Best Local Similarity   85.0%;  Pred. No. 3.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              |||||||||||  | |  ||||
Db         99 GGTGCATCGATCCTGTGGGG 80


RESULT 12
US-09-252-991A-7138/c
; Sequence 7138, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7138
;   LENGTH: 1584
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7138

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 1584;
  Best Local Similarity   85.0%;  Pred. No. 3.7e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              || |||  ||||||||||  ||
Db       1521 GGCGCAGCGATGCAGGGTGG 1502


RESULT 13
US-09-252-991A-7259/c
; Sequence 7259, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7259
;   LENGTH: 1794
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7259

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 1794;
  Best Local Similarity   85.0%;  Pred. No. 3.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              || |||  ||||||||||  ||
Db        208 GGCGCAGCGATGCAGGGTGG 189


RESULT 14
US-09-252-991A-7359
; Sequence 7359, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7359
;   LENGTH: 1872
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7359

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 1872;
  Best Local Similarity   85.0%;  Pred. No. 3.8e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy          1 GGTGCATCGATGCAGGGGGG 20
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Db        271 GGCGCAGCGATGCAGGGTGG 290


RESULT 15
US-09-949-016-12144
; Sequence 12144, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12144
;   LENGTH: 47199
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12144

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 47199;
  Best Local Similarity   85.0%;  Pred. No. 5.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
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Db       1520 GGTGCATCGATCCTGTGGGG 1539


Search completed: April 29, 2005, 12:02:28
Job time : 61.6385 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 268.243 Seconds
(without alignments)
453.893 Million cell updates/sec

Title: US-10-068-160A-1
Perfect score: 20
Sequence: 1 ggtgcatcgatgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	11	US-09-874-991C-494	Sequence 494, App
2	20	100.0	20	11	US-09-874-991C-505	Sequence 505, App
3	20	100.0	20	11	US-09-874-991C-538	Sequence 538, App
4	20	100.0	20	14	US-10-068-160-1	Sequence 1, Appli
5	20	100.0	20	14	US-10-068-160-54	Sequence 54, Appl
6	20	100.0	20	15	US-10-194-035-32	Sequence 32, Appl
7	20	100.0	20	15	US-10-194-035-34	Sequence 34, Appl
8	20	100.0	20	15	US-10-194-035-37	Sequence 37, Appl
9	20	100.0	20	15	US-10-194-035-38	Sequence 38, Appl
10	20	100.0	20	15	US-10-194-035-43	Sequence 43, Appl
11	20	100.0	20	15	US-10-194-035-72	Sequence 72, Appl
12	20	100.0	20	18	US-10-666-022-176	Sequence 176, App
13	20	100.0	20	18	US-10-666-022-177	Sequence 177, App
14	20	100.0	20	18	US-10-730-776-6	Sequence 6, Appli
15	20	100.0	20	18	US-10-730-776-7	Sequence 7, Appli
16	20	100.0	20	18	US-10-486-755-1	Sequence 1, Appli
17	20	100.0	20	18	US-10-486-755-15	Sequence 15, Appl
18	20	100.0	20	18	US-10-486-755-16	Sequence 16, Appl
19	20	100.0	20	18	US-10-486-755-22	Sequence 22, Appl
20	20	100.0	20	19	US-10-499-597-12	Sequence 12, Appl
21	20	100.0	20	19	US-10-499-597-38	Sequence 38, Appl
22	20	100.0	20	19	US-10-865-245-70	Sequence 70, Appl
23	20	100.0	22	11	US-09-874-991C-500	Sequence 500, App
24	20	100.0	22	11	US-09-874-991C-544	Sequence 544, App
25	20	100.0	28	11	US-09-874-991C-515	Sequence 515, App
26	20	100.0	28	11	US-09-874-991C-527	Sequence 527, App
27	20	100.0	29	11	US-09-874-991C-533	Sequence 533, App
28	20	100.0	30	11	US-09-874-991C-521	Sequence 521, App
29	20	100.0	30	11	US-09-874-991C-526	Sequence 526, App
30	20	100.0	32	11	US-09-874-991C-463	Sequence 463, App
31	20	100.0	32	18	US-10-486-755-29	Sequence 29, Appl
32	20	100.0	32	18	US-10-486-755-30	Sequence 30, Appl
33	20	100.0	32	18	US-10-486-755-31	Sequence 31, Appl
34	19	95.0	19	15	US-10-194-035-53	Sequence 53, Appl
35	19	95.0	19	15	US-10-194-035-73	Sequence 73, Appl
36	18.4	92.0	20	11	US-09-874-991C-498	Sequence 498, App
37	18.4	92.0	20	11	US-09-874-991C-499	Sequence 499, App
38	18.4	92.0	20	11	US-09-874-991C-509	Sequence 509, App
39	18.4	92.0	20	11	US-09-874-991C-510	Sequence 510, App
40	18.4	92.0	20	11	US-09-874-991C-542	Sequence 542, App
41	18.4	92.0	20	11	US-09-874-991C-543	Sequence 543, App
42	18.4	92.0	20	14	US-10-068-160-7	Sequence 7, Appli
43	18.4	92.0	20	14	US-10-068-160-11	Sequence 11, Appl
44	18.4	92.0	20	14	US-10-068-160-21	Sequence 21, Appl
45	18.4	92.0	20	14	US-10-068-160-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-874-991C-494
; Sequence 494, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-494

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GGTGCATCGATGCAGGGGGG 20
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RESULT 2

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US-09-874-991C-505
; Sequence 505, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 505
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-505

  Query Match             100.0%;  Score 20;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 3
US-09-874-991C-538
; Sequence 538, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-538

  Query Match             100.0%;  Score 20;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 4
US-10-068-160-1
; Sequence 1, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-1

  Query Match             100.0%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 5
US-10-068-160-54
; Sequence 54, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-54

  Query Match             100.0%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 6
US-10-194-035-32
; Sequence 32, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
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; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-32

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
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Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 7
US-10-194-035-34
; Sequence 34, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-34

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
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Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 8
US-10-194-035-37
; Sequence 37, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-37

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 9
US-10-194-035-38
; Sequence 38, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-38

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 10
US-10-194-035-43
; Sequence 43, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken

```
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-43

  Query Match             100.0%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 11
US-10-194-035-72
; Sequence 72, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-72

  Query Match             100.0%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 12
US-10-666-022-176
; Sequence 176, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISE
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-666-022-176

  Query Match             100.0%;  Score 20;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 13
US-10-666-022-177
; Sequence 177, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISE
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-666-022-177

  Query Match             100.0%;  Score 20;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCATCGATGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCATCGATGCAGGGGGG 20


RESULT 14
US-10-730-776-6
; Sequence 6, Application US/10730776
; Publication No. US20040213808A1
; GENERAL INFORMATION:
;  APPLICANT: Lieberman, Michael
;  APPLICANT:  Clements, David
;  APPLICANT:  Ogata, Steven
;  APPLICANT:  Nakano, Eileen
;  APPLICANT:  Leung, Julia
;  APPLICANT:  Humphreys, Tom
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; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST FLAVIVIRUS
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: 247332001100
; CURRENT APPLICATION NUMBER: US/10/730,776
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 60/432,865
; PRIOR FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: 60/493,312
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligodeoxyribonucleotide
US-10-730-776-6

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

RESULT 15
US-10-730-776-7
; Sequence 7, Application US/10730776
; Publication No. US20040213808A1
; GENERAL INFORMATION:
; APPLICANT: Lieberman, Michael
; APPLICANT: Clements, David
; APPLICANT: Ogata, Steven
; APPLICANT: Nakano, Eileen
; APPLICANT: Leung, Julia
; APPLICANT: Humphreys, Tom
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST FLAVIVIRUS
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: 247332001100
; CURRENT APPLICATION NUMBER: US/10/730,776
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 60/432,865
; PRIOR FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: 60/493,312
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligodeoxyribonucleotide
US-10-730-776-7

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCATCGATGCAGGGGGG 20

Search completed: April 29, 2005, 12:35:40
Job time : 270.243 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 791.351 Seconds
(without alignments)
1224.620 Million cell updates/sec

Title: US-10-068-160A-2
Perfect score: 20
Sequence: 1 ggtgcaccggtgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AX194442	AX194442 Sequence
2	20	100.0	20	6	AX352200	AX352200 Sequence
3	20	100.0	20	6	AX352208	AX352208 Sequence
4	20	100.0	20	6	AX352211	AX352211 Sequence
5	20	100.0	20	6	AX352218	AX352218 Sequence
6	20	100.0	20	6	AX352244	AX352244 Sequence
7	20	100.0	20	6	AX465392	AX465392 Sequence
8	20	100.0	28	6	AX352221	AX352221 Sequence
9	20	100.0	28	6	AX352229	AX352229 Sequence
10	20	100.0	28	6	AX352233	AX352233 Sequence
11	20	100.0	28	6	AX352241	AX352241 Sequence
12	20	100.0	40	6	AX352252	AX352252 Sequence
13	18.4	92.0	20	6	AX194501	AX194501 Sequence
14	18.4	92.0	20	6	AX352199	AX352199 Sequence
15	18.4	92.0	20	6	AX352203	AX352203 Sequence
16	18.4	92.0	20	6	AX352210	AX352210 Sequence
17	18.4	92.0	20	6	AX352214	AX352214 Sequence
18	18.4	92.0	20	6	AX352247	AX352247 Sequence
19	18.4	92.0	28	6	AX352220	AX352220 Sequence
20	18.4	92.0	28	6	AX352224	AX352224 Sequence
21	18.4	92.0	28	6	AX352232	AX352232 Sequence
22	18.4	92.0	28	6	AX352236	AX352236 Sequence
23	17.4	87.0	19	6	AX194422	AX194422 Sequence
24	17.4	87.0	19	6	AX465372	AX465372 Sequence
25	17.4	87.0	89713	1	AJ605139	AJ605139 Actinopla
c 26	17.4	87.0	155724	4	AC091316	AC091316 Sus scrof
c 27	17.4	87.0	170523	9	AP002387	AP002387 Homo sapi
28	17.4	87.0	187364	10	AC012295	AC012295 Mus muscu
29	17.4	87.0	203635	9	AC148310	AC148310 Pan trogl
30	17.4	87.0	233804	10	AC130831	AC130831 Mus muscu
31	17.4	87.0	238358	10	AL592465	AL592465 Mouse DNA
c 32	17.4	87.0	240647	10	AC131745	AC131745 Mus muscu
33	17	85.0	10782	1	AE001002	AE001002 Archaeogl
c 34	17	85.0	138859	9	AL359076	AL359076 Human DNA
35	16.8	84.0	20	6	AX194432	AX194432 Sequence
36	16.8	84.0	20	6	AX194434	AX194434 Sequence
37	16.8	84.0	20	6	AX194437	AX194437 Sequence
38	16.8	84.0	20	6	AX194438	AX194438 Sequence
39	16.8	84.0	20	6	AX194443	AX194443 Sequence
40	16.8	84.0	20	6	AX194472	AX194472 Sequence
41	16.8	84.0	20	6	AX194503	AX194503 Sequence
42	16.8	84.0	20	6	AX194504	AX194504 Sequence
43	16.8	84.0	20	6	AX352198	AX352198 Sequence
44	16.8	84.0	20	6	AX352209	AX352209 Sequence
45	16.8	84.0	20	6	AX352242	AX352242 Sequence

ALIGNMENTS

RESULT 1
AX194442
LOCUS AX194442 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 42 from Patent WO0151500.
ACCESSION AX194442
VERSION AX194442.1 GI:15385098
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 42 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
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Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 2
AX352200
LOCUS AX352200 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 496 from Patent WO0193902.
ACCESSION AX352200
VERSION AX352200.1 GI:18617483
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 496 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 3
AX352208
LOCUS       AX352208                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 504 from Patent WO0193902.
ACCESSION   AX352208
VERSION     AX352208.1  GI:18617491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 504 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 4
AX352211
LOCUS       AX352211                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 507 from Patent WO0193902.
ACCESSION   AX352211
VERSION     AX352211.1  GI:18617494
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 507 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 5
AX352218
LOCUS       AX352218                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 514 from Patent WO0193902.
ACCESSION   AX352218
VERSION     AX352218.1  GI:18617501
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 514 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 6
AX352244
LOCUS       AX352244                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 540 from Patent WO0193902.
ACCESSION   AX352244
VERSION     AX352244.1  GI:18617527
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 540 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
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Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 7
AX465392
LOCUS       AX465392                 20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 60 from Patent WO0211761.
ACCESSION   AX465392
VERSION     AX465392.1  GI:21899755
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 60 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 8
AX352221
LOCUS       AX352221                 28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 517 from Patent WO0193902.
ACCESSION   AX352221
VERSION     AX352221.1  GI:18617504
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 517 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 9
AX352229
LOCUS       AX352229                 28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 525 from Patent WO0193902.
ACCESSION   AX352229
VERSION     AX352229.1  GI:18617512
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 525 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .28
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 10
AX352233
LOCUS       AX352233                 28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 529 from Patent WO0193902.
ACCESSION   AX352233
VERSION     AX352233.1  GI:18617516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 529 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .28
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                     /note="Synthetic HDR"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          9 GGTGCACCGGTGCAGGGGGG 28


RESULT 11
AX352241
LOCUS       AX352241                 28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 537 from Patent WO0193902.
ACCESSION   AX352241
VERSION     AX352241.1  GI:18617524
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
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  JOURNAL   Patent: WO 0193902-A 537 13-DEC-2001;
            Biosynexus Incorporated (US)
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                     /note="Synthetic HDR"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          9 GGTGCACCGGTGCAGGGGGG 28


RESULT 12
AX352252
LOCUS       AX352252                  40 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 548 from Patent WO0193902.
ACCESSION   AX352252
VERSION     AX352252.1  GI:18617535
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 548 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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                     /note="Synthetic HDR"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 6;  Length 40;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db         14 GGTGCACCGGTGCAGGGGGG 33


RESULT 13
AX194501
LOCUS       AX194501                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 101 from Patent WO0151500.
ACCESSION   AX194501
VERSION     AX194501.1  GI:15385157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 101 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 8.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||| ||||||||||
Db          1 GGTGCACCGATGCAGGGGGG 20


RESULT 14
AX352199
LOCUS       AX352199                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 495 from Patent WO0193902.
ACCESSION   AX352199
VERSION     AX352199.1  GI:18617482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 495 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 8.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              |||||| ||||||||||||||
Db          1 GGTGCAGCGGTGCAGGGGGG 20


RESULT 15
AX352203
LOCUS       AX352203                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 499 from Patent WO0193902.
ACCESSION   AX352203
VERSION     AX352203.1  GI:18617486
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 499 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 8.6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||| ||||||||||
Db          1 GGTGCACCGATGCAGGGGGG 20
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Job time : 793.476 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 203.919 Seconds
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Title: US-10-068-160A-2
Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	4	AAC80622	Aac80622 Immunogen
2	20	100.0	20	4	AAS09592	Aas09592 Immunorea
3	20	100.0	20	6	ABL35614	Abl35614 Immunosti
4	20	100.0	20	6	ABL35578	Abl35578 Immunosti
5	20	100.0	20	6	ABL35581	Abl35581 Immunosti
6	20	100.0	20	6	ABL35570	Abl35570 Immunosti
7	20	100.0	20	6	ABL35588	Abl35588 Immunosti
8	20	100.0	20	6	ABK46470	Abk46470 Immunosti
9	20	100.0	20	8	ACC48296	Acc48296 CpG oligo
10	20	100.0	20	8	ACC48313	Acc48313 CpG oligo
11	20	100.0	20	9	ACC83118	Acc83118 D class C
12	20	100.0	20	9	ACC83152	Acc83152 D class O
13	20	100.0	20	10	ADD01049	Add01049 CpG D oli
14	20	100.0	20	12	ADN97044	Adn97044 Immunosti
15	20	100.0	28	6	ABL35599	Abl35599 Immunosti
16	20	100.0	28	6	ABL35603	Abl35603 Immunosti
17	20	100.0	28	6	ABL35591	Abl35591 Immunosti
18	20	100.0	28	6	ABL35611	Abl35611 Immunosti
19	20	100.0	40	6	ABL35622	Abl35622 Immunosti
20	18.4	92.0	20	4	AAS09651	Aas09651 Immunorea
21	18.4	92.0	20	6	ABL35573	Abl35573 Immunosti
22	18.4	92.0	20	6	ABL35584	Abl35584 Immunosti
23	18.4	92.0	20	6	ABL35569	Abl35569 Immunosti
24	18.4	92.0	20	6	ABL35617	Abl35617 Immunosti
25	18.4	92.0	20	6	ABL35580	Abl35580 Immunosti
26	18.4	92.0	20	8	ACC48311	Acc48311 CpG oligo
27	18.4	92.0	20	8	ACC48320	Acc48320 CpG oligo
28	18.4	92.0	20	8	ACC48321	Acc48321 CpG oligo
29	18.4	92.0	20	9	ACC83125	Acc83125 D class C
30	18.4	92.0	20	9	ACC83116	Acc83116 D class C
31	18.4	92.0	20	9	ACC83126	Acc83126 D class C
32	18.4	92.0	20	10	ADD01076	Add01076 CpG D oli
33	18.4	92.0	20	10	ADD01059	Add01059 CpG D oli
34	18.4	92.0	28	6	ABL35590	Abl35590 Immunosti
35	18.4	92.0	28	6	ABL35594	Abl35594 Immunosti
36	18.4	92.0	28	6	ABL35606	Abl35606 Immunosti
37	18.4	92.0	28	6	ABL35602	Abl35602 Immunosti
38	18	90.0	20	8	ACC48300	Acc48300 CpG oligo
39	18	90.0	20	12	ADN96868	Adn96868 Immunosti
40	17.4	87.0	19	4	AAC80602	Aac80602 Immunogen
41	17.4	87.0	19	4	AAS09572	Aas09572 Immunorea
42	17.4	87.0	19	6	ABK46450	Abk46450 Immunosti
43	16.8	84.0	20	4	AAC80652	Aac80652 Immunogen
44	16.8	84.0	20	4	AAC80722	Aac80722 Immunogen
45	16.8	84.0	20	4	AAC80614	Aac80614 Immunogen

ALIGNMENTS

RESULT 1
AAC80622
ID AAC80622 standard; DNA; 20 BP.
XX
AC AAC80622;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX

PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 2
AAS09592
ID AAS09592 standard; DNA; 20 BP.
XX
AC AAS09592;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #42.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 34; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 3
ABL35614
ID ABL35614 standard; DNA; 20 BP.
XX
AC ABL35614;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 540.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.

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XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 62; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 4
ABL35578
ID   ABL35578 standard; DNA; 20 BP.
XX
AC   ABL35578;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 504.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 5
ABL35581
ID   ABL35581 standard; DNA; 20 BP.
XX
AC   ABL35581;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 507.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
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FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 6
ABL35570
ID   ABL35570 standard; DNA; 20 BP.
XX
AC   ABL35570;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 496.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 7
ABL35588
ID   ABL35588 standard; DNA; 20 BP.
XX
AC   ABL35588;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 514.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
```

PN WO200193902-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018276.
XX
PR 07-JUN-2000; 2000US-0209797P.
XX
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Klinman DM;
XX
DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 61; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 8
ABK46470
ID ABK46470 standard; DNA; 20 BP.
XX
AC ABK46470;
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodideoxynucleotide #60.
XX
KW unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.
XX
PN WO200211761-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US041633.
XX
PR 10-AUG-2000; 2000US-0224011P.
PR 01-SEP-2000; 2000US-0229307P.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Mond JJ, Prince G, Klinman DM;
XX
DR WPI; 2002-227118/28.
XX
PT Vaccine for immunizing patient against respiratory syncytial virus, has
PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT linked by phosphate bond-oligodideoxynucleotides.
XX
PS Claim 4; Page 8; 30pp; English.
XX
CC The invention describes a vaccine comprising one or more epitopes of a
CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC vaccine is useful for vaccinating a patient especially against viruses of
CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC primary cause of viral bronchiolitis and pneumonia in infants and
CC children, and infectious pulmonary disease in infants. RSV has been
CC particularly implicated in death of infants that are premature, have
CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC represents an oligodideoxynucleotide that can be used in the creation of
CC the vaccine
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 9
ACC48296
ID ACC48296 standard; DNA; 20 BP.
XX
AC ACC48296;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide D29 used for dendritic cell maturation.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotides"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotide"
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX

PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Claim 11; Page 44; 69pp; English.
XX
CC The present sequence is that of D type CpG oligodeoxynucleotide D29,
CC which is used in a claimed method for generating a mature dendritic cell.
CC The method involves contacting a dendritic cell precursor, especially a
CC monocyte, with the oligonucleotide. The method is useful for generating
CC mature dendritic cells and enhancing T cell responses, thus enhancing
CC antigen presentation. Mature dendritic cells are useful for tumour
CC immunotherapy, for augmenting an immune response to an infectious agent
CC or to a vaccine, and as vaccines to prevent future infection or to
CC activate the immune system to treat diseases such as cancer. Mature
CC dendritic cells may also be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 10
ACC48313
ID ACC48313 standard; DNA; 20 BP.
XX
AC ACC48313;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Disclosure; Page 61; 69pp; English.
XX
CC The present sequence is that of a CpG oligodeoxynucleotide of the
CC invention. A claimed method for generating dendritic cells involves
CC contacting a dendritic cell precursor, especially a monocyte, with a D
CC type oligodeoxynucleotide (see ACC48294) containing a central
CC unmethylated CpG motif. The method is useful for generating mature
CC dendritic cells and enhancing T cell responses, thus enhancing antigen
CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
CC for augmenting an immune response to an infectious agent or to a vaccine,
CC and as vaccines to prevent future infection or to activate the immune
CC system to treat diseases such as cancer. Mature dendritic cells may also
CC be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 11
ACC83118
ID ACC83118 standard; DNA; 20 BP.
XX
AC ACC83118;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.
XX
OS Unidentified.
XX
PN WO2003040308-A2.
XX
PD 15-MAY-2003.
XX
PF 29-JUL-2002; 2002WO-US024235.
XX
PR 27-JUL-2001; 2001US-0308283P.
PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10C; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and

```
CC   multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC   ODN potentially useful for encapsulating in SSCL
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 12
ACC83152
ID   ACC83152 standard; DNA; 20 BP.
XX
AC   ACC83152;
XX
DT   27-AUG-2003  (first entry)
XX
DE   D class ODN sequence useful for encapsulating in SSCL, D29.
XX
KW   Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW   tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW   thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW   schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW   asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW   CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW   multiple sclerosis; infection; tumour; phosphorothioate backbone; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    16. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone"
XX
PN   WO2003040308-A2.
XX
PD   15-MAY-2003.
XX
PF   29-JUL-2002; 2002WO-US024235.
XX
PR   27-JUL-2001; 2001US-0308283P.
PR   25-JUL-2002; 2002US-00206407.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel I,  Ishii KJ,  Kawakami K,  Joshi BH,  Puri RK;
XX
DR   WPI; 2003-482260/45.
XX
PT   Cationic liposome composition for delivering oligodeoxynucleotides
PT   including a CpG motif in clinical applications, comprises a cationic
PT   lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS   Example 8; Page 52; 110pp; English.
XX
CC   The invention relates to sterically stabilised cationic liposomes (SSCL)
CC   which comprises a cationic lipid, a co-lipid, stabilising agent and
CC   encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC   The invention is useful in pharmaceutical composition for impairing
CC   growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC   interleukin-13 receptor in a subject; for stimulating an immune response,
CC   which is expression of a cytokine (e.g. interferon gamma), particularly
CC   immunotherapeutic response against tumours or stimulating an in vivo or
CC   an in vitro immune cell, and for inducing an immune response against an
CC   infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC   delivering oligodeoxynucleotides including a CpG motif in clinical
CC   applications; for treating infectious diseases (e.g. tularemia, malaria,
CC   francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC   (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC   etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC   bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC   diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC   multiple sclerosis) and psoriasis. The present sequence is a D class ODN
CC   potentially useful for encapsulating in SSCL
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 13
ADD01049
ID   ADD01049 standard; DNA; 20 BP.
XX
AC   ADD01049;
XX
DT   01-JAN-2004  (first entry)
XX
DE   CpG D oligonucleotide SEQ ID NO:13.
XX
KW   vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW   neovascularisation; angiogenesis; vulnerary; vasotropic;
KW   antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW   atherosclerosis; ischaemia; ss.
XX
OS   Synthetic.
XX
PN   WO2003054161-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US040955.
XX
PR   20-DEC-2001; 2001US-0343457P.
XX
PA   (UYTE-) UNIV TENNESSEE RES CORP.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Zheng M,  Rouse BT;
XX
DR   WPI; 2003-559138/52.
XX
PT   Inducing the production of vascular endothelial growth factor by a cell,
PT   useful for inducing angiogenesis, comprises contacting the cell with a
PT   CpG oligodeoxynucleotide.
XX
PS   Example 7; SEQ ID NO 13; 37pp; English.
XX
CC   The present invention describes a method for inducing the production of
CC   vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC   the cell with a CpG oligonucleotide and therefore inducing the production
CC   of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC   tissue, comprising introducing a CpG oligonucleotide into an area of the
CC   tissue where the formation of new blood vessels is desired, and so
CC   inducing neovascularisation in the area of the tissue; (2) promoting
CC   angiogenesis in an area of the subject where angiogenesis is desired,
CC   comprising introducing a CpG oligonucleotide to the area, and so
CC   promoting angiogenesis in the subject; and (3) screening for an agent
CC   that inhibits neovascularisation, comprising administering a CpG
CC   oligonucleotide to a non-human mammal and administering the agent to the
CC   mammal, where inhibition of angiogenesis in the animal indicates that the
CC   agent is effective in inhibiting neovascularisation. The CpG
CC   oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The method and the CpG
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CC   oligonucleotides can be used in inducing angiogenesis or
CC   neovascularisation, such as in subjects with a skin graft, subjects who
CC   exhibit male pattern baldness, or subjects who have a wound or who have
CC   atherosclerosis or ischaemia. The method may also be used in screening
CC   for agents that inhibit neovascularisation. The present sequence
CC   represents a CpG oligonucleotide which is used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 10;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 14
ADN97044
ID   ADN97044 standard; DNA; 20 BP.
XX
AC   ADN97044;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Immunostimulatory CpG oligonucleotide D29 seqid 178.
XX
KW   virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;
KW   tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;
KW   dermatological; bacterial growth inhibitor; immunostimulator;
KW   immune response; immunostimulatory; opportunistic infection;
KW   lentivirus infection; human immunodeficiency virus infection; AIDS;
KW   Leishmania infection; bacterial infection; fungal infection;
KW   viral infection; protozoan infection; prion disease; nucleoplasm;
KW   salmonellosis; syphilis; neurosyphilis; tuberculosis;
KW   bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;
KW   cryptococcal meningitis; hepatitis B; histoplasmosis; cryptosporidiosis;
KW   isosporiasis; microsporidiosis; pneumocystis carinii pneumonia;
KW   toxoplasmosis; cytomegalovirus; hepatitis; herpes simplex; herpes zoster;
KW   human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;
KW   progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;
KW   systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;
KW   HSV; genital herpes; HZV; shingles; genital wart; cervical cancer;
KW   immunostimulatory CpG oligonucleotide; ss.
XX
OS   Synthetic.
XX
PN   US2004105872-A1.
XX
PD   03-JUN-2004.
XX
PF   17-SEP-2003; 2003US-00666022.
XX
PR   18-SEP-2002; 2002US-0411944P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Verthelyi D;
XX
DR   WPI; 2004-419442/39.
XX
PT   Increasing an immune response to an opportunistic infection e.g.
PT   bacterial infections in an immunocompromised subject involves
PT   administering immunostimulatory D oligodeoxynucleotide or an
PT   immunostimulatory K oligodeoxynucleotide.
XX
PS   Example 8; SEQ ID NO 178; 64pp; English.
XX
CC   The invention describes a method of increasing an immune response to an
CC   opportunistic infection in an immunocompromised subject involves
CC   administering an immunostimulatory D oligodeoxynucleotide or an
CC   immunostimulatory K oligodeoxynucleotide, where an antigenic epitope of a
CC   polypeptide is not administered to the subject. The method is useful for
CC   increasing an immune response to an opportunistic infection e.g.
CC   infection with a lentivirus such as human immunodeficiency virus
CC   (including HIV-1, HIV-2) e.g. AIDS; infection with Leishmania; bacterial
CC   infections; fungal infections; viral infections; protozoan infections;
CC   prion disease; and nucleoplasm in an immunocompromised subject or a
CC   subject infected with a lentivirus. The bacterial infections include
CC   salmonellosis, syphilis and neurosyphilis, tuberculosis and bacillary
CC   angiomatosis, the fungal infections include aspergillosis, candidiasis,
CC   coccidioidomycosis, cryptococcal meningitis, hepatitis B, and
CC   histoplasmosis, the protozoal infections include cryptosporidiosis,
CC   isosporiasis, microsporidiosis, pneumocystis carinii pneumonia and
CC   toxoplasmosis, viral infections include cytomegalovirus, hepatitis,
CC   herpes simplex, herpes zoster, human papilloma virus, molluscum
CC   contagiosum, oral hairy leukoplakia and progressive multifocal
CC   leukoencephalopathy and neoplasms include Kaposi's sarcoma, systemic non-
CC   Hodgkin's lymphoma and primary central nervous system lymphoma. The
CC   herpes simplex includes HSV, genital herpes. The herpes zoster includes
CC   HZV and shingles. The human papilloma virus includes HPV, genital warts
CC   and cervical cancer. The method stimulates immune responses to any
CC   opportunistic infection in immunocompromised subjects. This sequence
CC   represents an immunostimulatory D CpG oligonucleotide sequence that
CC   stimulate the release of cytokines from cells of the immune system and
CC   can be used to increase immune response in the method of the invention.
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 12;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 15
ABL35599
ID   ABL35599 standard; DNA; 28 BP.
XX
AC   ABL35599;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 525.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .28
FT                   /*tag= a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
```

XX
DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX
PS Example 11; Page 61; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 28 BP; 10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCACCGGTGCAGGGGGG 20

Search completed: April 29, 2005, 06:25:59
Job time : 203.919 secs

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1875.14 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-2
Perfect score: 20
Sequence: 1 ggtgcaccggtgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.4	92.0	339	6	CB076094	CB076094 hf37c06.g
c	2	18.4	92.0	440	6	CB087291	CB087291 hj98g11.g
c	3	18.4	92.0	509	6	CB087214	CB087214 hj97e04.g
c	4	18.4	92.0	598	6	CB087525	CB087525 hk03f05.g
	5	18.4	92.0	840	9	CG271799	CG271799 OG0DZ26TV
	6	17.4	87.0	610	9	CG692380	CG692380 ZMMBBb029
c	7	17.4	87.0	779	8	CC109078	CC109078 NDL.50B23
c	8	17.4	87.0	799	8	CC133230	CC133230 NDL.50B22
	9	17.4	87.0	1005	9	CNS040Z1	AL269542 Tetraodon
c	10	17.4	87.0	1028	9	CL466773	CL466773 SAIL_1261
	11	17.4	87.0	1157	5	BX426076	BX426076 BX426076
c	12	17.4	87.0	1214	5	BQ898390	BQ898390 AGENCOURT
c	13	17	85.0	354	1	AV393217	AV393217 AV393217
	14	17	85.0	594	7	CO665888	CO665888 DG33-105o
c	15	16.8	84.0	54	9	CR086950	CR086950 Reverse s
	16	16.8	84.0	142	2	BE388878	BE388878 601284657
c	17	16.8	84.0	237	8	AZ492326	AZ492326 1M0326G23
	18	16.8	84.0	275	2	BB496626	BB496626 BB496626
c	19	16.8	84.0	289	1	AV219401	AV219401 AV219401
c	20	16.8	84.0	294	5	BY103614	BY103614 BY103614
	21	16.8	84.0	323	1	AL898002	AL898002 AL898002
c	22	16.8	84.0	338	7	CO781791	CO781791 BL013B_F0
c	23	16.8	84.0	383	8	BZ782509	BZ782509 A2SP3C56
	24	16.8	84.0	402	9	CE182406	CE182406 tigr-gss-
	25	16.8	84.0	421	1	AL897989	AL897989 AL897989
	26	16.8	84.0	430	8	BZ422920	BZ422920 hz32b02.g
c	27	16.8	84.0	442	7	CN963723	CN963723 11220_100
c	28	16.8	84.0	465	1	AJ684878	AJ684878 AJ684878
c	29	16.8	84.0	513	9	CE284352	CE284352 tigr-gss-
	30	16.8	84.0	562	1	AI370313	AI370313 qv76e01.x
	31	16.8	84.0	615	4	BJ252893	BJ252893 BJ252893
c	32	16.8	84.0	618	2	BE973745	BE973745 601680739
c	33	16.8	84.0	619	6	CD771763	CD771763 AGENCOURT
	34	16.8	84.0	630	8	BZ335826	BZ335826 hz27b01.g
c	35	16.8	84.0	631	4	BJ244833	BJ244833 BJ244833
c	36	16.8	84.0	646	6	CA100132	CA100132 SCVPCL604
c	37	16.8	84.0	646	9	CE419868	CE419868 tigr-gss-
c	38	16.8	84.0	665	7	CN788545	CN788545 4122892 B
	39	16.8	84.0	671	4	BJ229325	BJ229325 BJ229325
	40	16.8	84.0	675	7	CO691720	CO691720 DG11-36k2
c	41	16.8	84.0	677	8	BH886902	BH886902 LB01110a.
c	42	16.8	84.0	684	4	BM624520	BM624520 170006874
	43	16.8	84.0	685	4	BJ634520	BJ634520 BJ634520
c	44	16.8	84.0	692	4	BM620160	BM620160 170006874
	45	16.8	84.0	697	4	BJ250701	BJ250701 BJ250701

ALIGNMENTS

RESULT 1
CB076094/c
LOCUS CB076094 339 bp mRNA linear EST 24-JAN-2003
DEFINITION hf37c06.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis terminalis cDNA clone hf37c06, mRNA sequence.
ACCESSION CB076094
VERSION CB076094.1 GI:27889531
KEYWORDS EST.
SOURCE Hedyotis terminalis
ORGANISM Hedyotis terminalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Rubiaceae; Rubioideae; Spermacoceae; Hedyotis.
REFERENCE 1 (bases 1 to 339)
AUTHORS Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D.
TITLE Expressed tag sequences from Hedyotis terminalis flower - Stage 2 (NYBG)
JOURNAL Unpublished (2003)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hf37 row: c column: 06
Seq primer: -21M13UnivRev
High quality sequence stop: 339.
FEATURES Location/Qualifiers
source 1. .339
/organism="Hedyotis terminalis"
/mol_type="mRNA"
/db_xref="taxon:219667"
/clone="hf37c06"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date: Completed 12/18/01. Submitted to CSHL 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TM2562"
ORIGIN

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  Query Match             92.0%;  Score 18.4;  DB 6;  Length 339;
  Best Local Similarity   95.0%;  Pred. No. 6.7e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| ||||||||||||
Db         99 GGTGCACTGGTGCAGGGGGG 80


RESULT 2
CB087291/c
LOCUS       CB087291                440 bp    mRNA    linear   EST 27-JAN-2003
DEFINITION  hj98g11.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
            centranthoides cDNA clone hj98g11, mRNA sequence.
ACCESSION   CB087291
VERSION     CB087291.1  GI:27911483
KEYWORDS    EST.
SOURCE      Hedyotis centranthoides
  ORGANISM  Hedyotis centranthoides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
            Spermacoceae; Hedyotis.
REFERENCE   1  (bases 1 to 440)
  AUTHORS   Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P. and Stevenson,D.
  TITLE     Expressed tag sequences from Hedyotis centranthoides flower - Stage
            2 (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hj98  row: g  column: 11
            Seq primer: -21M13UnivRev
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .440
                     /organism="Hedyotis centranthoides"
                     /mol_type="mRNA"
                     /db_xref="taxon:219666"
                     /clone="hj98g11"
                     /dev_stage="pre-anthesis; Stage 2"
                     /clone_lib="Hedyotis centranthoides flower - Stage 2
                     (NYBG)"
                     /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
                     Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
                     CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
                     Synthesis Kit. The library was size-fractionated to enrich
                     for large inserts. Sample: collected on the island of
                     Hawaii, Hawaii; NYBG herbarium voucher TM2563"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 440;
  Best Local Similarity   95.0%;  Pred. No. 6.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| ||||||||||||
Db        131 GGTGCACTGGTGCAGGGGGG 112


RESULT 3
CB087214/c
LOCUS       CB087214                509 bp    mRNA    linear   EST 27-JAN-2003
DEFINITION  hj97e04.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
            centranthoides cDNA clone hj97e04, mRNA sequence.
ACCESSION   CB087214
VERSION     CB087214.1  GI:27911406
KEYWORDS    EST.
SOURCE      Hedyotis centranthoides
  ORGANISM  Hedyotis centranthoides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
            Spermacoceae; Hedyotis.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P. and Stevenson,D.
  TITLE     Expressed tag sequences from Hedyotis centranthoides flower - Stage
            2 (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hj97  row: e  column: 04
            Seq primer: -21M13UnivRev
            High quality sequence stop: 509.
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Hedyotis centranthoides"
                     /mol_type="mRNA"
                     /db_xref="taxon:219666"
                     /clone="hj97e04"
                     /dev_stage="pre-anthesis; Stage 2"
                     /clone_lib="Hedyotis centranthoides flower - Stage 2
                     (NYBG)"
                     /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
                     Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
                     CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
                     Synthesis Kit. The library was size-fractionated to enrich
                     for large inserts. Sample: collected on the island of
                     Hawaii, Hawaii; NYBG herbarium voucher TM2563"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 509;
  Best Local Similarity   95.0%;  Pred. No. 6.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| ||||||||||||
Db        146 GGTGCACTGGTGCAGGGGGG 127


RESULT 4
CB087525/c
LOCUS       CB087525                598 bp    mRNA    linear   EST 27-JAN-2003
DEFINITION  hk03f05.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
            centranthoides cDNA clone hk03f05, mRNA sequence.
ACCESSION   CB087525
VERSION     CB087525.1  GI:27911717
KEYWORDS    EST.
SOURCE      Hedyotis centranthoides
  ORGANISM  Hedyotis centranthoides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
            Spermacoceae; Hedyotis.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P. and Stevenson,D.
  TITLE     Expressed tag sequences from Hedyotis centranthoides flower - Stage
            2 (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
```

```
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hk03  row: f  column: 05
            Seq primer: -21M13UnivRev
            High quality sequence stop: 598.
FEATURES             Location/Qualifiers
     source          1. .598
                     /organism="Hedyotis centranthoides"
                     /mol_type="mRNA"
                     /db_xref="taxon:219666"
                     /clone="hk03f05"
                     /dev_stage="pre-anthesis; Stage 2"
                     /clone_lib="Hedyotis centranthoides flower - Stage 2
                     (NYBG)"
                     /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
                     Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
                     CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
                     Synthesis Kit. The library was size-fractionated to enrich
                     for large inserts. Sample: collected on the island of
                     Hawaii, Hawaii; NYBG herbarium voucher TM2563"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 598;
  Best Local Similarity   95.0%;  Pred. No. 6.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| ||||||||||||
Db        148 GGTGCACTGGTGCAGGGGGG 129


RESULT 5
CG271799
LOCUS       CG271799                840 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG0DZ26TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0696F04,
            genomic survey sequence.
ACCESSION   CG271799
VERSION     CG271799.1  GI:34183940
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG0DZ26TH
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0696F04"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 9;  Length 840;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              || ||||||||||||||||
Db        499 GGCGCACCGGTGCAGGGGGG 518


RESULT 6
CG692380
LOCUS       CG692380                610 bp    DNA     linear   GSS 14-OCT-2003
DEFINITION  ZMMBBb0292G11.f ZMMBBb Zea mays genomic clone ZMMBBb0292G11 5',
            genomic survey sequence.
ACCESSION   CG692380
VERSION     CG692380.1  GI:37656062
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
            and Wing,R.
  TITLE     Sequencing of the maize genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: M13r
            Plate: 0292  row: G  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBb0292G11"
                     /lab_host="DH10B"
                     /clone_lib="ZMMBBb"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Zea mays L. ssp. mays"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 9;  Length 610;
  Best Local Similarity   94.7%;  Pred. No. 1.9e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              |||||||||| ||||||||
Db        524 GTGCACCGGTTCAGGGGGG 542


RESULT 7
CC109078/c
LOCUS       CC109078                779 bp    DNA     linear   GSS 16-APR-2003
DEFINITION  NDL.50B23.T7 Notre Dame Liverpool Aedes aegypti genomic clone
            NDL.50B23, genomic survey sequence.
ACCESSION   CC109078
VERSION     CC109078.1  GI:29978133
KEYWORDS    GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
```

```
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 779)
  AUTHORS   Loftus,B., Shetty,J., Knudson,D. and Severson,D.
  TITLE     BAC end sequencing of Aedes aegypti
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: NDL.50B23.SP6
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@tigr.org
            Library was provided by David Severson
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .779
                     /organism="Aedes aegypti"
                     /mol_type="genomic DNA"
                     /strain="Liverpool"
                     /db_xref="taxon:7159"
                     /clone="NDL.50B23"
                     /clone_lib="Notre Dame Liverpool"
                     /note="Vector: pECBAC1; Site_1: Hind III; The library was
                     prepared from whole body tissue of newly hatched L1 larvae
                     by David Severson at the University of Notre Dame and
                     Hongbin Zhang"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 8;  Length 779;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              ||||||||||||||| ||||
Db        307 GTGCACCGGTGCAGTGGGG 289


RESULT 8
CC133230/c
LOCUS       CC133230                799 bp    DNA     linear   GSS 16-APR-2003
DEFINITION  NDL.50B22.T7 Notre Dame Liverpool Aedes aegypti genomic clone
            NDL.50B22, genomic survey sequence.
ACCESSION   CC133230
VERSION     CC133230.1  GI:30002285
KEYWORDS    GSS.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 799)
  AUTHORS   Loftus,B., Shetty,J., Knudson,D. and Severson,D.
  TITLE     BAC end sequencing of Aedes aegypti
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: NDL.50B22.SP6
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@tigr.org
            Library was provided by David Severson
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .799
                     /organism="Aedes aegypti"
                     /mol_type="genomic DNA"
                     /strain="Liverpool"
                     /db_xref="taxon:7159"
                     /clone="NDL.50B22"
                     /clone_lib="Notre Dame Liverpool"
                     /note="Vector: pECBAC1; Site_1: Hind III; The library was
                     prepared from whole body tissue of newly hatched L1 larvae
                     by David Severson at the University of Notre Dame and
                     Hongbin Zhang"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 8;  Length 799;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              ||||||||||||||| ||||
Db        307 GTGCACCGGTGCAGTGGGG 289


RESULT 9
CNS040Z1
LOCUS       CNS040Z1                1005 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            073O18 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL269542
VERSION     AL269542.1  GI:7991434
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 1005)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1005
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="073O18"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG073BH09SP1~end :
                     PUC-Ori"
ORIGIN
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  Query Match             87.0%;  Score 17.4;  DB 9;  Length 1005;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              |||| ||||||||||||||||
Db         84 GTGCTCCGGTGCAGGGGGG 102


RESULT 10
CL466773/c
LOCUS       CL466773                1028 bp    DNA     linear   GSS 31-MAR-2004
DEFINITION  SAIL_1261_B06.v1 SAIL Collection Arabidopsis thaliana genomic clone
            SAIL_1261_B06.v1, genomic survey sequence.
ACCESSION   CL466773
VERSION     CL466773.1  GI:45869678
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1028)
  AUTHORS   Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
            Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
            Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
            Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
  TITLE     A high-throughput Arabidopsis reverse genetics system
  JOURNAL   Plant Cell 14 (12), 2985-2994 (2002)
  MEDLINE   22356987
   PUBMED   12468722
COMMENT     Contact: Sessions A
            Applied Trait Genetics
            Syngenta Biotechnology Inc.
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS846660; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
            single contiguous sequences.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .1028
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="SAIL_1261_B06.v1"
                     /clone_lib="SAIL Collection"
                     /note="T-DNA left border sequences were isolated using a
                     modified TAIL-PCR strategy"
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 9;  Length 1028;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGG 19
              |||||||||||||| |||||
Db        887 GGTGCACCGGTGCCGGGGG 869


RESULT 11
BX426076
LOCUS       BX426076                1157 bp    mRNA    linear   EST 04-MAY-2004
DEFINITION  BX426076 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF009YC20 5-PRIME, mRNA sequence.
ACCESSION   BX426076
VERSION     BX426076.2  GI:47002199
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1157)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30774523.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 1373.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0AAW15ZA08QP1&c=1373.r.
FEATURES             Location/Qualifiers
     source          1. .1157
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF009YC20"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 5;  Length 1157;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGG 19
              || ||||||||||||||||
Db       1075 GGGGCACCGGTGCAGGGGG 1093


RESULT 12
BQ898390/c
LOCUS       BQ898390                1214 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8712137 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295181
            5', mRNA sequence.
ACCESSION   BQ898390
VERSION     BQ898390.1  GI:22290404
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1214)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2501  row: a  column: 06
            High quality sequence stop: 150.
FEATURES             Location/Qualifiers
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     source          1. .1214
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6295181"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             87.0%;  Score 17.4;  DB 5;  Length 1214;
  Best Local Similarity   94.7%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGG 19
              ||||||||| |||||||||
Db        301 GGTGCACCGATGCAGGGGG 283


RESULT 13
AV393217/c
LOCUS       AV393217                354 bp    mRNA    linear   EST 23-APR-2002
DEFINITION  AV393217 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
            cDNA clone CM097f03_r 5', mRNA sequence.
ACCESSION   AV393217
VERSION     AV393217.1  GI:6547433
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
  TITLE     A large scale structural analysis of cDNAs in a unicellular green
            alga, Chlamydomonas reinhardtii. I. Generation of 3433
            non-redundant expressed sequence tags
  JOURNAL   DNA Res. 6 (6), 369-373 (1999)
  MEDLINE   20152988
   PUBMED   10691129
COMMENT     Contact: Yasukazu Nakamura
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .354
                     /organism="Chlamydomonas reinhardtii"
                     /mol_type="mRNA"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="CM097f03_r"
                     /dev_stage="photoautotrophic growth"
                     /clone_lib="Chlamydomonas reinhardtii C9"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGG 17
              |||||||||||||||||
Db        310 GGTGCACCGGTGCAGGG 294


RESULT 14
CO665888
LOCUS       CO665888                594 bp    mRNA    linear   EST 26-JUL-2004
DEFINITION  DG33-105o6 DG33-aorta Canis familiaris cDNA 3', mRNA sequence.
ACCESSION   CO665888
VERSION     CO665888.1  GI:50605135
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
            Henrich,J. and Loebbert,R.
  TITLE     Dog arrayTAG cDNA clone collection
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Thomas Schlueter
            LION bioscience AG
            Waldhoferstrasse 98, D-69123 Heidelberg, Germany
            Tel: +49 6221 4038 150
            Fax: +49 6221 4038 290
            Email: Thomas.Schlueter@lionbioscience.com.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /strain="Beagle"
                     /db_xref="taxon:9615"
                     /tissue_type="aorta"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="DG33-aorta"
                     /note="Organ: aorta; Vector: Dog pBluescript LION"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 7;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCACCGGTGCAGGGGGG 20
              |||||||||||||||||
Db        536 GCACCGGTGCAGGGGGG 552


RESULT 15
CR086950/c
LOCUS       CR086950                 54 bp    DNA     linear   GSS 05-JUL-2004
DEFINITION  Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHPP370o19, genomic survey sequence.
ACCESSION   CR086950
VERSION     CR086950.1  GI:49820542
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPP370o19"
                     /clone_lib="MHPP"
ORIGIN
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Query Match 84.0%; Score 16.8; DB 9; Length 54;
Best Local Similarity 90.0%; Pred. No. 3.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GGTGCACCGGTGCAGGGGGG 20
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Db         35 GATGCTCCGGTGCAGGGGGG 16
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Search completed: April 29, 2005, 11:55:12
Job time : 1878.14 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 58.5135 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-2
Perfect score: 20
Sequence: 1 ggtgcaccggtgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	16.8	84.0	601	4	US-09-949-016-19926	Sequence 19926, A
	2	16.8	84.0	601	4	US-09-949-016-46188	Sequence 46188, A
	3	16.8	84.0	22927	4	US-09-949-016-11849	Sequence 11849, A
	4	16.8	84.0	22928	4	US-09-949-016-13071	Sequence 13071, A
c	5	16.8	84.0	38653	4	US-09-922-445-1	Sequence 1, Appli
	6	15.8	79.0	288	4	US-09-270-767-26956	Sequence 26956, A
	7	15.8	79.0	633	4	US-09-489-039A-2752	Sequence 2752, Ap
	8	15.8	79.0	2255	4	US-09-270-767-11388	Sequence 11388, A
	9	15.8	79.0	3358	3	US-09-248-571-2	Sequence 2, Appli
	10	15.8	79.0	3358	3	US-09-553-736-2	Sequence 2, Appli
c	11	15.8	79.0	7353	4	US-09-949-016-14895	Sequence 14895, A
	12	15.8	79.0	10627	1	US-08-060-925A-12	Sequence 12, Appl
	13	15.8	79.0	12222	4	US-09-328-925-42	Sequence 42, Appl
	14	15.8	79.0	36938	4	US-09-949-016-13484	Sequence 13484, A
	15	15.4	77.0	366	4	US-09-489-039A-5836	Sequence 5836, Ap
c	16	15.4	77.0	1446	4	US-09-902-540-5188	Sequence 5188, Ap
	17	15.4	77.0	34199	4	US-09-902-540-1255	Sequence 1255, Ap
	18	15.2	76.0	480	4	US-09-252-991A-5639	Sequence 5639, Ap
c	19	15.2	76.0	564	4	US-09-252-991A-5555	Sequence 5555, Ap
	20	15.2	76.0	601	4	US-09-949-016-20059	Sequence 20059, A
	21	15.2	76.0	601	4	US-09-949-016-84902	Sequence 84902, A
	22	15.2	76.0	601	4	US-09-949-016-105107	Sequence 105107,
	23	15.2	76.0	601	4	US-09-949-016-174099	Sequence 174099,
	24	15.2	76.0	601	4	US-09-949-016-174100	Sequence 174100,
c	25	15.2	76.0	774	4	US-09-252-991A-5590	Sequence 5590, Ap
	26	15.2	76.0	1083	3	US-09-655-270A-20	Sequence 20, Appl
	27	15.2	76.0	1098	3	US-09-651-941-24	Sequence 24, Appl
	28	15.2	76.0	1098	3	US-09-955-597-24	Sequence 24, Appl
	29	15.2	76.0	1432	4	US-09-902-540-264	Sequence 264, App
	30	15.2	76.0	1432	4	US-09-902-540-6080	Sequence 6080, Ap
	31	15.2	76.0	3296	4	US-09-902-540-651	Sequence 651, App
c	32	15.2	76.0	4320	4	US-09-902-540-577	Sequence 577, App
c	33	15.2	76.0	4320	4	US-09-902-540-6854	Sequence 6854, Ap
	34	15.2	76.0	12508	3	US-09-655-270A-1	Sequence 1, Appli
	35	15.2	76.0	12523	3	US-09-651-941-1	Sequence 1, Appli
	36	15.2	76.0	12523	3	US-09-955-597-1	Sequence 1, Appli
	37	15.2	76.0	13675	4	US-09-949-016-11746	Sequence 11746, A
c	38	15.2	76.0	15206	4	US-09-949-016-13585	Sequence 13585, A
c	39	15.2	76.0	15206	4	US-09-949-016-13586	Sequence 13586, A
	40	15.2	76.0	24707	4	US-09-740-027-3	Sequence 3, Appli
	41	15.2	76.0	24720	4	US-09-949-016-12341	Sequence 12341, A
	42	15.2	76.0	24721	4	US-09-949-016-15610	Sequence 15610, A
c	43	15.2	76.0	30054	4	US-09-949-016-16429	Sequence 16429, A
	44	15.2	76.0	31300	4	US-09-949-016-16967	Sequence 16967, A
c	45	15.2	76.0	34539	4	US-09-949-016-12226	Sequence 12226, A

ALIGNMENTS

RESULT 1
US-09-949-016-19926
; Sequence 19926, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19926
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19926

Query Match 84.0%; Score 16.8; DB 4; Length 601;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| || |||||||||
Db        310 GGTGCACTGGGGCAGGGGGG 329
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RESULT 2
US-09-949-016-46188
; Sequence 46188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

```
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46188
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-46188

  Query Match             84.0%;  Score 16.8;  DB 4;  Length 601;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| || |||||||||
Db        310 GGTGCACTGGGGCAGGGGGG 329


RESULT 3
US-09-949-016-11849
; Sequence 11849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11849
;   LENGTH: 22927
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11849

  Query Match             84.0%;  Score 16.8;  DB 4;  Length 22927;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| || |||||||||
Db       7140 GGTGCACTGGGGCAGGGGGG 7159


RESULT 4
US-09-949-016-13071
; Sequence 13071, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13071
;   LENGTH: 22928
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13071

  Query Match             84.0%;  Score 16.8;  DB 4;  Length 22928;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| || |||||||||
Db       7140 GGTGCACTGGGGCAGGGGGG 7159


RESULT 5
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
;  APPLICANT: Andersson, Maria K.
;  APPLICANT:  Berglund, Lars G. T.
;  APPLICANT:  Reneland, Rikard  H.
;  APPLICANT:  Adam, Gail I. R.
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
;  FILE REFERENCE: GG126US
;  CURRENT APPLICATION NUMBER: US/09/922,445
;  CURRENT FILING DATE:  2001-08-03
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 38653
;   TYPE: DNA
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(26156)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (24801)..(24801)
;   OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can b
;   OTHER INFORMATION: A or G
;   NAME/KEY: misc_feature
;   LOCATION: (24941)..(24941)
;   OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can b
;   OTHER INFORMATION: T or C
;   NAME/KEY: exon
;   LOCATION: (26157)..(26252)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (26253)..(26401)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (26402)..(26543)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (26544)..(27024)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (27025)..(27178)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (27179)..(30519)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (27645)..(27645)
;   OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can b
;   OTHER INFORMATION: C or G
;   NAME/KEY: exon
;   LOCATION: (30520)..(30681)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (30682)..(30894)
;   OTHER INFORMATION:
;   NAME/KEY: exon
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;   LOCATION: (30895)..(31027)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (31028)..(31747)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (31748)..(31841)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (31842)..(32400)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (32163)..(32163)
;   OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: A or C
;   NAME/KEY: exon
;   LOCATION: (32401)..(32528)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (32529)..(33414)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (32614)..(32614)
;   OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
;   OTHER INFORMATION: A or G
;   NAME/KEY: exon
;   LOCATION: (33415)..(33597)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (33598)..(34314)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (34315)..(34588)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (34589)..(36404)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (36405)..(36523)
;   OTHER INFORMATION:
;   NAME/KEY: Intron
;   LOCATION: (36524)..(38341)
;   OTHER INFORMATION:
;   NAME/KEY: exon
;   LOCATION: (38342)..(38653)
;   OTHER INFORMATION:
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Genbank/AC004923
;   DATABASE ENTRY DATE: 1999-12-21
;   RELEVANT RESIDUES: (1)..(38653)
US-09-922-445-1

  Query Match             84.0%;  Score 16.8;  DB 4;  Length 38653;
  Best Local Similarity   90.0%;  Pred. No. 1.7e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||| || |||||||||
Db      14714 GGTGCACTGGGGCAGGGGGG 14695


RESULT 6
US-09-270-767-26956
; Sequence 26956, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26956
;   LENGTH: 288
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-26956

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 288;
  Best Local Similarity   89.5%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGG 19
              |||||| |||||||| |||
Db        110 GGTGCATCGGTGCAGTGGG 128


RESULT 7
US-09-489-039A-2752
; Sequence 2752, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 2752
;   LENGTH: 633
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2752

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 633;
  Best Local Similarity   89.5%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGG 19
              ||||| |||||||||||| |
Db        614 GGTGCGCCGGTGCAGGGTG 632


RESULT 8
US-09-270-767-11388
; Sequence 11388, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11388
;   LENGTH: 2255
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-11388

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 2255;
  Best Local Similarity   89.5%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGG 19
              |||||| |||||||| |||
Db        110 GGTGCATCGGTGCAGTGGG 128


RESULT 9
US-09-248-571-2
```

```
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
;  APPLICANT: BASBAUM, CAROL
;  APPLICANT: GALLUP, MARIANNE
;  APPLICANT: DAIZONG, LI
;  APPLICANT: GEBREMICHAEL, ASSEFA
;  APPLICANT: GENSCH, ERIN
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
;  TITLE OF INVENTION: GENE EXPRESSION
;  FILE REFERENCE: UCSF12/02
;  CURRENT APPLICATION NUMBER: US/09/248,571
;  CURRENT FILING DATE: 1999-02-11
;  EARLIER APPLICATION NUMBER: 60/074,398
;  EARLIER FILING DATE: 1998-02-11
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 3358
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-248-571-2

  Query Match             79.0%;  Score 15.8;  DB 3;  Length 3358;
  Best Local Similarity   89.5%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              ||||||| ||||||||||
Db        998 GTGCACCCATGCAGGGGGG 1016


RESULT 10
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
;  APPLICANT:  BASBAUM, Carol
;  APPLICANT:  GALLUP, Marianne
;  APPLICANT:  DAIZONG, Li
;  APPLICANT:  GEBREMICHAEL, Assefa
;  APPLICANT:  GENSCH, Erin
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
;  TITLE OF INVENTION:  MUCIN GENE EXPRESSION
;  FILE REFERENCE:  UCSF-012/03US
;  CURRENT APPLICATION NUMBER: US/09/553,736
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER:  US 09/248,571
;  PRIOR FILING DATE:  1999-02-11
;  PRIOR APPLICATION NUMBER:  US 60/074,398
;  PRIOR FILING DATE:  1998-02-11
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3358
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-553-736-2

  Query Match             79.0%;  Score 15.8;  DB 3;  Length 3358;
  Best Local Similarity   89.5%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              |||||||| ||||||||||
Db        998 GTGCACCCATGCAGGGGGG 1016


RESULT 11
US-09-949-016-14895/c
; Sequence 14895, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14895
;   LENGTH: 7353
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(7353)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14895

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 7353;
  Best Local Similarity   89.5%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTGCACCGGTGCAGGGGGG 20
              | ||| ||||||||||||||
Db        647 GGGCAGCGGTGCAGGGGGG 629


RESULT 12
US-08-060-925A-12
; Sequence 12, Application US/08060925A
; Patent No. 5439824
;  GENERAL INFORMATION:
;    APPLICANT:  Brantley, Mark
;    APPLICANT:  Laubach, Victor
;    TITLE OF INVENTION:  INCREASED EXPRESSION OF ALPHA-1
;    TITLE OF INVENTION:  ANTITRYPSIN IN EXPRESSION VECTORS THROUGH THE INCLUSION OF
;    TITLE OF INVENTION:  INTRON II
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON AND BEAR
;      STREET:  620 NEWPORT CENTER DRIVE  SIXTEENTH FLOOR
;      CITY:  NEWPORT BEACH
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/060,925A
;      FILING DATE:  06-MAY-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fuller, Michael L.
;      REGISTRATION NUMBER:  36,516
;      REFERENCE/DOCKET NUMBER:  NIH040.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10627 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-060-925A-12

Query Match 79.0%; Score 15.8; DB 1; Length 10627;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GGTGCACCGGTGCAGGGGG 19
              ||||||||  | ||||||||
Db      10086 GGTGCACCTGAGCAGGGGG 10104
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RESULT 13
US-09-328-925-42
; Sequence 42, Application US/09328925
; Patent No. 6610906
; GENERAL INFORMATION:
; APPLICANT: Kurachi, Kotoku
; APPLICANT: Kurachi, Sumiko
; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UM-03603
; CURRENT APPLICATION NUMBER: US/09/328,925
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 12222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-42

Query Match 79.0%; Score 15.8; DB 4; Length 12222;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GGTGCACCGGTGCAGGGGG 19
              ||||||||  | ||||||||
Db      11680 GGTGCACCTGAGCAGGGGG 11698
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RESULT 14
US-09-949-016-13484
; Sequence 13484, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13484
; LENGTH: 36938
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13484

Query Match 79.0%; Score 15.8; DB 4; Length 36938;
Best Local Similarity 89.5%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 GTGCACCGGTGCAGGGGGG 20
                ||||||  |||||||||| |
Db      16008 GTGCACAGGTGCAGGGGTG 16026
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RESULT 15
US-09-489-039A-5836
; Sequence 5836, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5836
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5836

Query Match 77.0%; Score 15.4; DB 4; Length 366;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GGTGCACCGGTGCAGGG 17
              |||||||||| ||||||
Db         70 GGTGCACCGGCGCAGGG 86
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 268.243 Seconds
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Title: US-10-068-160A-2
Perfect score: 20
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Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	11	US-09-874-991C-496	Sequence 496, App
2	20	100.0	20	11	US-09-874-991C-504	Sequence 504, App
3	20	100.0	20	11	US-09-874-991C-507	Sequence 507, App
4	20	100.0	20	11	US-09-874-991C-514	Sequence 514, App
5	20	100.0	20	11	US-09-874-991C-540	Sequence 540, App
6	20	100.0	20	14	US-10-068-160-2	Sequence 2, Appli
7	20	100.0	20	15	US-10-194-035-42	Sequence 42, Appl
8	20	100.0	20	18	US-10-666-022-178	Sequence 178, App
9	20	100.0	20	18	US-10-486-755-2	Sequence 2, Appli
10	20	100.0	20	18	US-10-486-755-19	Sequence 19, Appl
11	20	100.0	20	19	US-10-499-597-13	Sequence 13, Appl
12	20	100.0	28	11	US-09-874-991C-517	Sequence 517, App
13	20	100.0	28	11	US-09-874-991C-525	Sequence 525, App
14	20	100.0	28	11	US-09-874-991C-529	Sequence 529, App
15	20	100.0	28	11	US-09-874-991C-537	Sequence 537, App
16	20	100.0	40	11	US-09-874-991C-548	Sequence 548, App
17	18.4	92.0	20	11	US-09-874-991C-495	Sequence 495, App
18	18.4	92.0	20	11	US-09-874-991C-499	Sequence 499, App
19	18.4	92.0	20	11	US-09-874-991C-506	Sequence 506, App
20	18.4	92.0	20	11	US-09-874-991C-510	Sequence 510, App
21	18.4	92.0	20	11	US-09-874-991C-543	Sequence 543, App
22	18.4	92.0	20	14	US-10-068-160-37	Sequence 37, Appl
23	18.4	92.0	20	14	US-10-068-160-58	Sequence 58, Appl
24	18.4	92.0	20	15	US-10-194-035-101	Sequence 101, App
25	18.4	92.0	20	18	US-10-486-755-17	Sequence 17, Appl
26	18.4	92.0	20	18	US-10-486-755-26	Sequence 26, Appl
27	18.4	92.0	20	18	US-10-486-755-27	Sequence 27, Appl
28	18.4	92.0	20	19	US-10-499-597-23	Sequence 23, Appl
29	18.4	92.0	20	19	US-10-499-597-40	Sequence 40, Appl
30	18.4	92.0	28	11	US-09-874-991C-516	Sequence 516, App
31	18.4	92.0	28	11	US-09-874-991C-520	Sequence 520, App
32	18.4	92.0	28	11	US-09-874-991C-528	Sequence 528, App
33	18.4	92.0	28	11	US-09-874-991C-532	Sequence 532, App
34	18	90.0	18	14	US-10-068-160-13	Sequence 13, Appl
35	18	90.0	20	18	US-10-666-022-2	Sequence 2, Appli
36	18	90.0	20	18	US-10-486-755-6	Sequence 6, Appli
37	17.4	87.0	19	15	US-10-194-035-22	Sequence 22, Appl
c 38	17.4	87.0	940	18	US-10-425-115-169731	Sequence 169731,
c 39	17	85.0	432	18	US-10-425-115-150828	Sequence 150828,
40	16.8	84.0	20	11	US-09-874-991C-494	Sequence 494, App
41	16.8	84.0	20	11	US-09-874-991C-505	Sequence 505, App
42	16.8	84.0	20	11	US-09-874-991C-538	Sequence 538, App
43	16.8	84.0	20	14	US-10-068-160-1	Sequence 1, Appli
44	16.8	84.0	20	14	US-10-068-160-5	Sequence 5, Appli
45	16.8	84.0	20	14	US-10-068-160-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-874-991C-496
; Sequence 496, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 496
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-496

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20
```

RESULT 2

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US-09-874-991C-504
; Sequence 504, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 504
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-504

  Query Match             100.0%;  Score 20;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 3
US-09-874-991C-507
; Sequence 507, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 507
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-507

  Query Match             100.0%;  Score 20;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 4
US-09-874-991C-514
; Sequence 514, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 514
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-514

  Query Match             100.0%;  Score 20;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 5
US-09-874-991C-540
; Sequence 540, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 540
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-540

  Query Match             100.0%;  Score 20;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 6
US-10-068-160-2
; Sequence 2, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
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;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-2

  Query Match             100.0%;  Score 20;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 7
US-10-194-035-42
; Sequence 42, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42

  Query Match             100.0%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 8
US-10-666-022-178
; Sequence 178, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 178
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-666-022-178

  Query Match             100.0%;  Score 20;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 9
US-10-486-755-2
; Sequence 2, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-486-755-2

  Query Match             100.0%;  Score 20;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 10
US-10-486-755-19
; Sequence 19, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
```

```
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-486-755-19

  Query Match            100.0%;  Score 20;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 11
US-10-499-597-13
; Sequence 13, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Rouse, Barry T.
;  APPLICANT:  Zheng, Mei
;  TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
;  FILE REFERENCE: 4239-64125-02
;  CURRENT APPLICATION NUMBER: US/10/499,597
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: PCT/US02/40955
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,457
;  PRIOR FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG D oligonucleotide
US-10-499-597-13

  Query Match            100.0%;  Score 20;  DB 19;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 12
US-09-874-991C-517
; Sequence 517, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-517

  Query Match            100.0%;  Score 20;  DB 11;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 13
US-09-874-991C-525
; Sequence 525, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-525

  Query Match            100.0%;  Score 20;  DB 11;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCACCGGTGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCACCGGTGCAGGGGGG 20


RESULT 14
US-09-874-991C-529
; Sequence 529, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-529

Query Match 100.0%; Score 20; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 9 GGTGCACCGGTGCAGGGGGG 28

RESULT 15
US-09-874-991C-537
; Sequence 537, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-537

Query Match 100.0%; Score 20; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 20
||||||||||||||||||||
Db 9 GGTGCACCGGTGCAGGGGGG 28

Search completed: April 29, 2005, 12:35:40
Job time : 268.243 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 712.216 Seconds
(without alignments)
1224.620 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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36	17	94.4	17	6	AX352205	AX352205 Sequence
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38	17	94.4	17	6	AX352249	AX352249 Sequence
39	17	94.4	17	6	AX352253	AX352253 Sequence
40	17	94.4	19	6	AX194453	AX194453 Sequence
41	17	94.4	19	6	AX194473	AX194473 Sequence
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44	17	94.4	25	6	AX352226	AX352226 Sequence
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ALIGNMENTS

RESULT 1
AX352207
LOCUS AX352207 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 503 from Patent WO0193902.
ACCESSION AX352207
VERSION AX352207.1 GI:18617490
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 503 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX352217 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 513 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 551 from Patent WO0193902.
ACCESSION   AX352255
VERSION     AX352255.1  GI:18617538
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 551 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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Qy          1 TGCATCGATGCAGGGGGG 18
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RESULT 4
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LOCUS       AX194432                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 32 from Patent WO0151500.
ACCESSION   AX194432
VERSION     AX194432.1  GI:15385088
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 32 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 82;
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 5
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LOCUS       AX194434                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 34 from Patent WO0151500.
ACCESSION   AX194434
VERSION     AX194434.1  GI:15385090
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 34 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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LOCUS       AX194437                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 37 from Patent WO0151500.
ACCESSION   AX194437
VERSION     AX194437.1  GI:15385093
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 37 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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RESULT 7
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LOCUS       AX194438                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 38 from Patent WO0151500.
ACCESSION   AX194438
VERSION     AX194438.1  GI:15385094
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 38 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 8
AX194443
LOCUS       AX194443                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 43 from Patent WO0151500.
ACCESSION   AX194443
VERSION     AX194443.1  GI:15385099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 43 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 9
AX194472
LOCUS       AX194472                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 72 from Patent WO0151500.
ACCESSION   AX194472
VERSION     AX194472.1  GI:15385128
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 72 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 10
AX352198
LOCUS       AX352198                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 494 from Patent WO0193902.
ACCESSION   AX352198
VERSION     AX352198.1  GI:18617481
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 494 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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RESULT 11
AX352206
LOCUS       AX352206                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 502 from Patent WO0193902.
ACCESSION   AX352206
VERSION     AX352206.1  GI:18617489
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 502 13-DEC-2001;
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Db          3 TGCATCGATGCAGGGGGG 20


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DEFINITION  Sequence 505 from Patent WO0193902.
ACCESSION   AX352209
VERSION     AX352209.1  GI:18617492
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 505 13-DEC-2001;
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 13
AX352216
LOCUS       AX352216                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 512 from Patent WO0193902.
ACCESSION   AX352216
VERSION     AX352216.1  GI:18617499
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 512 13-DEC-2001;
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 14
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LOCUS       AX352242                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 538 from Patent WO0193902.
ACCESSION   AX352242
VERSION     AX352242.1  GI:18617525
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 538 13-DEC-2001;
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RESULT 15
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LOCUS       AX352250                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 546 from Patent WO0193902.
ACCESSION   AX352250
VERSION     AX352250.1  GI:18617533
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 546 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20
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Job time : 712.341 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 183.527 Seconds
(without alignments)
580.598 Million cell updates/sec

Title: US-10-068-160A-12
Perfect score: 18
Sequence: 1 tgcatcgatgcaggggggg 18

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Searched: 4390206 seqs, 2959870667 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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22	18	100.0	20	6	ABL35620	Abl35620 Immunosti
23	18	100.0	20	6	ABL35612	Abl35612 Immunosti
24	18	100.0	20	6	ABK46500	Abk46500 Immunosti
25	18	100.0	20	6	ABK46460	Abk46460 Immunosti
26	18	100.0	20	6	ABK46465	Abk46465 Immunosti
27	18	100.0	20	6	ABK46471	Abk46471 Immunosti
28	18	100.0	20	6	ABK46462	Abk46462 Immunosti
29	18	100.0	20	6	ABK46466	Abk46466 Immunosti
30	18	100.0	20	8	ACC48309	Acc48309 CpG oligo
31	18	100.0	20	8	ACC48295	Acc48295 CpG oligo
32	18	100.0	20	8	ACC48299	Acc48299 CpG oligo
33	18	100.0	20	8	ACC48310	Acc48310 CpG oligo
34	18	100.0	20	8	ACC48316	Acc48316 CpG oligo
35	18	100.0	20	9	ACC83150	Acc83150 D class O
36	18	100.0	20	9	ACC83115	Acc83115 D class C
37	18	100.0	20	9	ACC83151	Acc83151 D class O
38	18	100.0	20	9	ACC83114	Acc83114 D class C
39	18	100.0	20	9	ACC83121	Acc83121 D class C
40	18	100.0	20	10	ADB84186	Adb84186 CpG conta
41	18	100.0	20	10	ADC51789	Adc51789 D19 SEQ I
42	18	100.0	20	10	ADD01074	Add01074 CpG D oli
43	18	100.0	20	10	ADD01048	Add01048 CpG D oli
44	18	100.0	20	10	ADD01060	Add01060 CpG D oli
45	18	100.0	20	12	ADK67597	Adk67597 Immunosti

ALIGNMENTS

RESULT 1
ABL35587
ID ABL35587 standard; DNA; 18 BP.
XX
AC ABL35587;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 513.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .18
FT /*tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
PN WO200193902-A2.
XX
PD 13-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018276.
XX
PR 07-JUN-2000; 2000US-0209797P.
XX
PA (BIOS-) BIOSYNEXUS INC.
XX
PI Mond JJ, Flora M, Klinman DM;
XX
DR WPI; 2002-130570/17.
XX
PT New immunostimulatory compositions comprising RNA/DNA hybrid
PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.

```
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          1 TGCATCGATGCAGGGGGG 18


RESULT 2
ABL35577
ID   ABL35577 standard; DNA; 18 BP.
XX
AC   ABL35577;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 503.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .18
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          1 TGCATCGATGCAGGGGGG 18


RESULT 3
ABL35625
ID   ABL35625 standard; DNA; 18 BP.
XX
AC   ABL35625;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 551.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .18
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 62; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
```

CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 1 TGCATCGATGCAGGGGGG 18

RESULT 4
ADD01052
ID ADD01052 standard; DNA; 18 BP.
XX
AC ADD01052;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG D oligonucleotide SEQ ID NO:16.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerary; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
PN WO2003054161-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Zheng M, Rouse BT;
XX
DR WPI; 2003-559138/52.
XX
PT Inducing the production of vascular endothelial growth factor by a cell,
PT useful for inducing angiogenesis, comprises contacting the cell with a
PT CpG oligodeoxynucleotide.
XX
PS Example 7; SEQ ID NO 16; 37pp; English.
XX
CC The present invention describes a method for inducing the production of
CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC the cell with a CpG oligonucleotide and therefore inducing the production
CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC tissue, comprising introducing a CpG oligonucleotide into an area of the
CC tissue where the formation of new blood vessels is desired, and so
CC inducing neovascularisation in the area of the tissue; (2) promoting
CC angiogenesis in an area of the subject where angiogenesis is desired,
CC comprising introducing a CpG oligonucleotide to the area, and so
CC promoting angiogenesis in the subject; and (3) screening for an agent
CC that inhibits neovascularisation, comprising administering a CpG
CC oligonucleotide to a non-human mammal and administering the agent to the
CC mammal, where inhibition of angiogenesis in the animal indicates that the
CC agent is effective in inhibiting neovascularisation. The CpG
CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC activities, and can be used in gene therapy. The method and the CpG
CC oligonucleotides can be used in inducing angiogenesis or
CC neovascularisation, such as in subjects with a skin graft, subjects who
CC exhibit male pattern baldness, or subjects who have a wound or who have
CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a CpG oligonucleotide which is used in the exemplification of
CC the present invention.
XX
SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 1 TGCATCGATGCAGGGGGG 18

RESULT 5
AAC80652
ID AAC80652 standard; DNA; 20 BP.
XX
AC AAC80652;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:72.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 35; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides

CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 18;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20
```

RESULT 6
AAC80614
ID AAC80614 standard; DNA; 20 BP.
XX
AC AAC80614;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:34.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 29; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 18;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20
```

RESULT 7
AAC80612
ID AAC80612 standard; DNA; 20 BP.
XX
AC AAC80612;
XX
DT 14-FEB-2001 (first entry)

XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:32.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 29; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 8
AAC80617
ID AAC80617 standard; DNA; 20 BP.
XX
AC AAC80617;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:37.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 29; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells

CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 9
AAC80618
ID AAC80618 standard; DNA; 20 BP.
XX
AC AAC80618;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:38.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 10
AAC80623
ID AAC80623 standard; DNA; 20 BP.
XX
AC AAC80623;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:43.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
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PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
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CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 11
AAS09622
ID AAS09622 standard; DNA; 20 BP.
XX
AC AAS09622;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #72.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 39; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy: The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 18;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20
```

RESULT 12
AAS09582
ID AAS09582 standard; DNA; 20 BP.
XX
AC AAS09582;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #32.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 32; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 18;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20
```

RESULT 13
AAS09587
ID AAS09587 standard; DNA; 20 BP.
XX
AC AAS09587;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #37.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 33; 48pp; English.
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CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines

CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 14
AAS09593
ID AAS09593 standard; DNA; 20 BP.
XX
AC AAS09593;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #43.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 34; 48pp; English.
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CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 15
AAS09584
ID AAS09584 standard; DNA; 20 BP.
XX
AC AAS09584;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #34.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
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PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
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PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
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PS Claim 5; Page 32; 48pp; English.
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CC gamma (IFN-gamma) production or a humoral immune response involving B

CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20
```

Search completed: April 29, 2005, 06:26:00
Job time : 184.527 secs

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1687.62 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-12
Perfect score: 18
Sequence: 1 tgcatcgatgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	94.4	807	6	CA101677	SCACHR104
	2	16.4	91.1	240	1	AV281636	AV281636 AV281636
c	3	16.4	91.1	245	2	AW325275	AW325275 TENU4637
	4	16.4	91.1	257	1	AV268287	AV268287 AV268287
c	5	16.4	91.1	277	8	AQ444154	AQ444154 GSSTc0207
	6	16.4	91.1	303	1	AV269637	AV269637 AV269637
c	7	16.4	91.1	655	7	CO101616	GR__Eb002
c	8	16.4	91.1	665	7	CO075430	GR__Ea36C
	9	16.4	91.1	927	4	BI733127	BI733127 603354541
c	10	16.4	91.1	1014	9	AG056417	AG056417 Pan trogl
	11	16.4	91.1	1055	9	CNS05EI8	AL333737 Tetraodon
	12	16.4	91.1	1096	9	CNS05CPL	AL331410 Tetraodon
c	13	16	88.9	839	9	CG066914	PUIBJ87TD
	14	15.4	85.6	309	4	BM336824	BM336824 MEST199-D
	15	15.4	85.6	347	5	BP086394	BP086394 BP086394
	16	15.4	85.6	350	5	BQ405718	BQ405718 GA__Ed008
	17	15.4	85.6	362	2	BE053563	BE053563 GA__Ea002
	18	15.4	85.6	374	6	CB966250	CB966250 NL34_G07
	19	15.4	85.6	386	5	BQ405503	BQ405503 GA__Ed008
c	20	15.4	85.6	386	5	BQ414174	BQ414174 GA__Ed008
c	21	15.4	85.6	473	4	BI507147	BI507147 BB170025B
	22	15.4	85.6	522	6	CD725298	CD725298 MK_20_75
c	23	15.4	85.6	540	6	CA115848	CA115848 SCVPLB101
	24	15.4	85.6	550	6	CD668465	CD668465 eec1c.pk0
c	25	15.4	85.6	607	5	BQ815309	BQ815309 1030049F0
	26	15.4	85.6	616	4	BG446545	BG446545 GA__Eb003
c	27	15.4	85.6	617	5	BU654335	BU654335 1112112H0
c	28	15.4	85.6	621	8	BH450526	BH450526 BOGFX73TR
	29	15.4	85.6	626	4	BG444716	BG444716 GA__Ea002
	30	15.4	85.6	639	9	CE220284	CE220284 tigr-gss-
c	31	15.4	85.6	640	5	BQ825319	BQ825319 1030126A0
	32	15.4	85.6	656	6	CD308125	CD308125 StrPu691.
c	33	15.4	85.6	664	6	CA247902	CA247902 SCCCFL506
	34	15.4	85.6	670	8	BH996954	BH996954 oep83h09.
c	35	15.4	85.6	674	7	CO408283	CO408283 VRK464 Vi
c	36	15.4	85.6	679	8	BH577346	BH577346 BOGGD05TR
c	37	15.4	85.6	685	6	CA222223	CA222223 SCEZFL404
	38	15.4	85.6	688	2	BF276108	BF276108 GA__Eb002
c	39	15.4	85.6	691	7	CN036520	CN036520 nm_16_b9_
c	40	15.4	85.6	700	8	BH685253	BH685253 BOMMA43TR
c	41	15.4	85.6	702	8	BH471235	BH471235 BOGRT27TR
c	42	15.4	85.6	705	7	CO106974	CO106974 GR__Eb003
c	43	15.4	85.6	705	9	CL688248	CL688248 PRI0149a_
c	44	15.4	85.6	722	7	CO125145	CO125145 GR__Eb08H
c	45	15.4	85.6	732	7	CO116215	CO116215 GR__Eb018

ALIGNMENTS

RESULT 1
CA101677/c
LOCUS CA101677 807 bp mRNA linear EST 23-SEP-2003
DEFINITION SCACHR1040C03.g HR1 Saccharum officinarum cDNA clone SCACHR1040C03 5', mRNA sequence.
ACCESSION CA101677
VERSION CA101677.1 GI:34954984
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 807)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 040 row: C column: 03
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .807
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCACHR1040C03"
/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirilum rubrisubalbicans; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Herbaspirilum rubrisubalbicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details

of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 94.4%; Score 17; DB 6; Length 807;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 GCATCGATGCAGGGGGG 18
              |||||||||||||||||
Db         32 GCATCGATGCAGGGGGG 16
```

RESULT 2
AV281636
LOCUS AV281636 240 bp mRNA linear EST 05-NOV-1999
DEFINITION AV281636 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933425J05 3', mRNA sequence.
ACCESSION AV281636
VERSION AV281636.1 GI:6269673
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 240)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .240
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933425J05"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis (DH10B)"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN

Query Match 91.1%; Score 16.4; DB 1; Length 240;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCATCGATGCAGGGGGG 18
              |||||||| |||||||||
Db         85 TGCATCGAGGCAGGGGGG 102
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RESULT 3
AW325275/c
LOCUS AW325275 245 bp mRNA linear EST 21-SEP-2000
DEFINITION TENU4637 T.cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 25h9 5', mRNA sequence.
ACCESSION AW325275
VERSION AW325275.1 GI:6761196
KEYWORDS EST.
SOURCE Trypanosoma cruzi
ORGANISM Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum.
REFERENCE 1 (bases 1 to 245)
AUTHORS Porcel,B.M., Tran,A.-N., Tammi,M., Nyarady,Z., Rydaker,M., Urmenyi,T.P., Rondinelli,E., Pettersson,U., Andersson,B. and Aslund,L.
TITLE Gene survey of the pathogenic protozoan Trypanosoma cruzi
JOURNAL Genome Res. 10 (8), 1103-1107 (2000)
MEDLINE 20414748
PUBMED 10958628
COMMENT Contact: Aslund L
Department of Medical Genetics
Uppsala University
Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
Tel: 46 18 471 45 85
Fax: 46 18 52 68 49
Email: lena.aslund@medgen.uu.se
Seq primer: T7 primer
High quality sequence stop: 245.
FEATURES Location/Qualifiers
source 1. .245
/organism="Trypanosoma cruzi"
/mol_type="mRNA"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="25h9"
/cell_type="epimastigote"
/clone_lib="T.cruzi epimastigote normalized cDNA Library"
/note="cDNA library constructed with oligo dt primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker (Pharmacia)"

ORIGIN

Query Match 91.1%; Score 16.4; DB 2; Length 245;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;

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  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||| ||||||||||
Db         65 TGCATCGGTGCAGGGGGG 48


RESULT 4
AV268287
LOCUS       AV268287                257 bp    mRNA    linear   EST 05-NOV-1999
DEFINITION  AV268287 RIKEN full-length enriched, adult male testis (DH10B) Mus
            musculus cDNA clone 4930534F16 3', mRNA sequence.
ACCESSION   AV268287
VERSION     AV268287.1  GI:6256324
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 257)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
            Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .257
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="4930534F16"
                     /sex="male"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male testis
                     (DH10B)"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3']. cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 1;  Length 257;
  Best Local Similarity   94.4%;  Pred. No. 8.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||| |||||||||
Db         97 TGCATCGAGGCAGGGGGG 114


RESULT 5
AQ444154/c
LOCUS       AQ444154                277 bp    DNA     linear   GSS 09-JAN-2001
DEFINITION  GSSTc0207 Trypanosoma cruzi random genomic library Trypanosoma
            cruzi genomic clone G10L7, genomic survey sequence.
ACCESSION   AQ444154
VERSION     AQ444154.3  GI:10130745
KEYWORDS    GSS.
SOURCE      Trypanosoma cruzi
  ORGANISM  Trypanosoma cruzi
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma; Schizotrypanum.
REFERENCE   1  (bases 1 to 277)
  AUTHORS   Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
  TITLE     A random sequencing approach for the analysis of the trypanosoma
            cruzi genome: general structure, large gene and repetitive DNA
            families, and gene discovery
  JOURNAL   Genome Res. 10 (12), 1996-2005 (2000)
  MEDLINE   20568489
   PUBMED   11116094
COMMENT     On Sep 14, 2000 this sequence version replaced gi:9372108.
            Contact: Sanchez D.O.
            Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
            Aires, Argentina
            Tel: (54-11) 4580/7255/7
            Fax: (54-11) 4752-9639
            Email: dsanchez@iib.unsam.edu.ar
            Sequences were basecalled with phred and vector was masked with
            crossmatch (see http://genome.washington.edu). Sequences were then
            trimmed from both ends to remove low quality bases and masked
            vector.
            Seq primer: T7
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .277
                     /organism="Trypanosoma cruzi"
                     /mol_type="genomic DNA"
                     /strain="CL-Brener"
                     /db_xref="taxon:5693"
                     /clone="G10L7"
                     /cell_type="epimastigote"
                     /clone_lib="Trypanosoma cruzi random genomic library"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
                     randomly sheared using a nebulizer and the 1 to 2 Kb range
                     was gel purified and cloned into the dephosphoryated
                     HincII site of the vector"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 8;  Length 277;
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  Best Local Similarity   94.4%;  Pred. No. 8.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||| ||||||||||
Db        238 TGCATCGGTGCAGGGGGG 221


RESULT 6
AV269637
LOCUS       AV269637               303 bp    mRNA    linear   EST 05-NOV-1999
DEFINITION  AV269637 RIKEN full-length enriched, adult male testis (DH10B) Mus
            musculus cDNA clone 4930544G09 3', mRNA sequence.
ACCESSION   AV269637
VERSION     AV269637.1  GI:6257674
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 303)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
            Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al. 1999)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
             Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .303
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="4930544G09"
                     /sex="male"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male testis
                     (DH10B)"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 1;  Length 303;
  Best Local Similarity   94.4%;  Pred. No. 8.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||||||| |||||||||
Db        143 TGCATCGAGGCAGGGGGG 160


RESULT 7
CO101616/c
LOCUS       CO101616               655 bp    mRNA    linear   EST 16-JUN-2004
DEFINITION  GR__Eb0028C17.f GR__Eb Gossypium raimondii cDNA clone GR__Eb0028C17
            5', mRNA sequence.
ACCESSION   CO101616
VERSION     CO101616.1  GI:48800302
KEYWORDS    EST.
SOURCE      Gossypium raimondii
  ORGANISM  Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 655)
  AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
  TITLE     Global assembly of Cotton ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            Plate: 0028  row: C  column: 17.
FEATURES             Location/Qualifiers
     source          1. .655
                     /organism="Gossypium raimondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:29730"
                     /clone="GR__Eb0028C17"
                     /tissue_type="floral"
                     /dev_stage="_3 to +3 DPA"
                     /lab_host="DH10B"
                     /clone_lib="GR__Eb"
                     /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
                     EcoRV; Library made by Invitrogen with RNA supplied by
                     Wendle lab. Directional cloned into NotI-EV. Colonies
                     plated/picked by AGI. More glycerol clones held in -80."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 7;  Length 655;
  Best Local Similarity   94.4%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||| |||||||
Db        198 TGCATCGATGTAGGGGGG 181
```

```
RESULT 8
CO075430/c
LOCUS       CO075430                665 bp    mRNA    linear   EST 15-JUN-2004
DEFINITION  GR__Ea36C02.f GR__Ea Gossypium raimondii cDNA clone GR__Ea36C02 5',
            mRNA sequence.
ACCESSION   CO075430
VERSION     CO075430.1  GI:48744911
KEYWORDS    EST.
SOURCE      Gossypium raimondii
  ORGANISM  Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 665)
  AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
  TITLE     Global assembly of Cotton ESTs
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            Plate: 36  row: C  column: 02.
FEATURES             Location/Qualifiers
     source          1. .665
                     /organism="Gossypium raimondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:29730"
                     /clone="GR__Ea36C02"
                     /tissue_type="whole seedlings"
                     /dev_stage="first true leaves"
                     /lab_host="DH10B"
                     /clone_lib="GR__Ea"
                     /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
                     EcoRV; Library made by Invitrogen with RNA supplied by
                     Wendle lab. Directional cloned into NotI-EV.  Colonies
                     plated/picked by AGI. More glycerol clones held in -80."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 7;  Length 665;
  Best Local Similarity   94.4%;  Pred. No. 9.3e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||||| ||||||||||
Db        596 TGCATCCATGCAGGGGGG 579


RESULT 9
BI733127
LOCUS       BI733127                927 bp    mRNA    linear   EST 20-SEP-2001
DEFINITION  603354541F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5361707 5',
            mRNA sequence.
ACCESSION   BI733127
VERSION     BI733127.1  GI:15710140
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11920  row: b  column: 12
            High quality sequence stop: 240.
FEATURES             Location/Qualifiers
     source          1. .927
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5361707"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_94"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 4;  Length 927;
  Best Local Similarity   94.4%;  Pred. No. 9.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||||| ||||||||||
Db        622 TGCATCTATGCAGGGGGG 639


RESULT 10
AG056417/c
LOCUS       AG056417                1014 bp    DNA     linear   GSS 02-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-042L04.F, genomic survey sequence.
ACCESSION   AG056417
VERSION     AG056417.1  GI:16593876
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1014)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                Sequencing: -21M13
             LIBRARY
                Vector    : pKS145
                R.Site 1  : SacI
                R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .1014
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-042L04.F"
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                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 1014;
  Best Local Similarity   94.4%;  Pred. No. 9.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||||| ||||||||||
Db         99 TGCATCCATGCAGGGGGG 82


RESULT 11
CNS05EI8
LOCUS       CNS05EI8                1055 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            014J04 of library C from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL333737
VERSION     AL333737.1  GI:8227495
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 1055)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1055
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="014J04"
                     /clone_lib="C"
                     /note="Genoscope sequence ID : C0TC014DE02C1~end : T7"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 1055;
  Best Local Similarity   94.4%;  Pred. No. 9.7e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||| ||||||||||
Db         33 TGCATCGCTGCAGGGGGG 50


RESULT 12
CNS05CPL
LOCUS       CNS05CPL                1096 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            021M06 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL331410
VERSION     AL331410.1  GI:8225119
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 1096)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1096
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="021M06"
                     /clone_lib="A"
                     /note="Genoscope sequence ID : C0AA021BG03C2~end : T7"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 1096;
  Best Local Similarity   94.4%;  Pred. No. 9.8e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||| ||||||||||
Db        427 TGCATCGCTGCAGGGGGG 444


RESULT 13
CG066914/c
LOCUS       CG066914                 839 bp    DNA     linear   GSS 19-AUG-2003
DEFINITION  PUIBJ87TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0544P06,
            genomic survey sequence.
ACCESSION   CG066914
VERSION     CG066914.1  GI:33939094
KEYWORDS    GSS.
```

```
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 839)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUIBJ87TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .839
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0544P06"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 9;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGG 16
              ||||||||||||||||
Db        123 TGCATCGATGCAGGGG 108


RESULT 14
BM336824
LOCUS       BM336824                309 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  MEST199-D06.T3 ISUM5-RN Zea mays cDNA clone MEST199-D06 3', mRNA
            sequence.
ACCESSION   BM336824
VERSION     BM336824.1  GI:18166985
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 309)
  AUTHORS   Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
  TITLE     Expressed Sequence Tags from B73 Maize: various stages and tissues
            including seedlings treated with a variety of hormones
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Patrick S. Schnable
            Schnable Laboratory
            Iowa State University
            G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
            Tel: 515-294-0975
            Fax: 515-294-2299
            Email: schnable@iastate.edu
            Individual basecall and confidence value were assigned using the
            Phred software,
            (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
            rt). Overall sequence quality assessment and vector trimming were
            conducted using the Lucy software (<http://www.tigr.org/softlab/>).
            Lucy parameters were set to ensure an overall trimmed quality of
            97.5% or better without any vector fragments in the chosen
            high-quality region of each sequence. Low-quality bases between the
            poly-T and the high-quality region were replaced with N's to serve
            as spacers.
            PCR PRimers
            FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
            BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
            Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES             Location/Qualifiers
     source          1. .309
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="MEST199-D06"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
                     /clone_lib="ISUM5-RN"
                     /note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
                     Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
                     Mixed mature tissures  (17, 21, 38, 69, 77 DAG), Kernels
                     (3, 5, 10, 15, 20, 25, 30, DAP),  Adventious roots (65
                     DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature  ear
                     (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk,
                     unpollinated  first ear, ear shank, etiolated seedlings,
                     callus, Cycloheximide-treated  callus, Anaerobic treated
                     seedlings, NAA (a-Naphthalene  acetic acid)-treated
                     seedlings, Kinetin-treated seedlings, ACPC
                     (1-aminocyclopropane-1-carboxylix acid)-treated seedlings,
                     Brassinolide-treated seedlings, ABA (Abscisic
                     acid)-treated seedlings, GA (Gibberellic acid)-treated
                     seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
                     molecules were generated as follows. First-strand cDNA was
                     prepared from oligo-dT selected mRNA by priming with a
                     NotI oligo-dT primer (5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT). The
                     resulting DNA:RNA hybrid was treated with RNase H and used
                     as a template for DNA PolI-catalyzed second strand
                     synthesis. After the addition of EcoRI adaptors, the
                     ds-cDNAs were digested with NotI and size-selected. The
                     resulting molecules were directionally cloned into the
                     EcoRI and NotI sites of the pT7T3PAC vector. The library
                     then went through one round of normalization to CoT value
                     of 5 based on the methods of Marcelo Bento Soares (Genome
                     Research 6: 791-806, 1996)."
ORIGIN

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 309;
  Best Local Similarity   94.1%;  Pred. No. 2.9e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGG 17
              |||||||||| ||||||
Db        180 TGCATCGATGGAGGGGG 196


RESULT 15
BP086394
LOCUS       BP086394                347 bp    mRNA    linear   EST 30-JUN-2004
DEFINITION  BP086394 Chlamydomonas reinhardtii C9 various conditions
            Chlamydomonas reinhardtii cDNA clone MX007h07_r 5', mRNA sequence.
ACCESSION   BP086394
VERSION     BP086394.1  GI:49458481
KEYWORDS    EST.
SOURCE      Chlamydomonas reinhardtii
  ORGANISM  Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1  (bases 1 to 347)
  AUTHORS   Asamizu,E., Nakamura,Y., Miura,K., Fukuzawa,H., Fujiwara,S.,
            Hirono,M., Iwamoto,K., Matsuda,Y., Minagawa,J., Shimogawara,K.,
            Takahashi,Y. and Tabata,S.
  TITLE     Establishment of Publicly Available cDNA Material and Information
            Resource of Chlamydomonas reinhardtii (Chlorophyta), to Facilitate
```

```
            Gene Function Analysis
  JOURNAL   Phycologia (2004) In press
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .347
                     /organism="Chlamydomonas reinhardtii"
                     /mol_type="mRNA"
                     /strain="C9"
                     /db_xref="taxon:3055"
                     /clone="MX007h07_r"
                     /clone_lib="Chlamydomonas reinhardtii C9 various
                     conditions"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was made from a mixture of cells
                     grown under various conditions"
ORIGIN

  Query Match             85.6%;  Score 15.4;  DB 5;  Length 347;
  Best Local Similarity   94.1%;  Pred. No. 3e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCATCGATGCAGGGGGG 18
              ||| |||||||||||||
Db        212 GCAGCGATGCAGGGGGG 228


Search completed: April 29, 2005, 11:55:15
Job time : 1690.62 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 52.6622 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-12
Perfect score: 18
Sequence: 1 tgcatcgatgcaggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
c	1	15.4	85.6	300598	4	US-09-949-016-11868	Sequence 11868, A
c	2	15.4	85.6	302604	4	US-09-949-016-14588	Sequence 14588, A
c	3	15.4	85.6	302604	4	US-09-949-016-14589	Sequence 14589, A
c	4	15.4	85.6	308362	4	US-09-949-016-17119	Sequence 17119, A
	5	14.8	82.2	3358	3	US-09-248-571-2	Sequence 2, Appli
	6	14.8	82.2	3358	3	US-09-553-736-2	Sequence 2, Appli
c	7	14.8	82.2	17032	4	US-09-949-016-12476	Sequence 12476, A
c	8	14.8	82.2	17032	4	US-09-949-016-13352	Sequence 13352, A
	9	14.8	82.2	37004	4	US-09-949-016-15317	Sequence 15317, A
c	10	14.8	82.2	131631	4	US-09-949-016-11757	Sequence 11757, A
	11	14.4	80.0	736	4	US-09-270-767-14521	Sequence 14521, A
c	12	14.4	80.0	1086	4	US-09-252-991A-13644	Sequence 13644, A
c	13	14.4	80.0	1092	4	US-09-252-991A-13444	Sequence 13444, A
	14	14.4	80.0	1194	4	US-09-252-991A-13697	Sequence 13697, A
c	15	14.4	80.0	4280	4	US-09-079-592-1	Sequence 1, Appli
c	16	14.4	80.0	5496	3	US-09-462-284-1	Sequence 1, Appli
c	17	14.4	80.0	26104	4	US-09-949-016-14045	Sequence 14045, A
c	18	14.4	80.0	32654	4	US-09-801-191A-3	Sequence 3, Appli
c	19	14.4	80.0	32654	4	US-10-345-198-3	Sequence 3, Appli
c	20	14.4	80.0	77626	4	US-09-949-016-12608	Sequence 12608, A
c	21	14.4	80.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
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	23	14.4	80.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	24	14.4	80.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	25	14	77.8	905	3	US-09-221-017B-560	Sequence 560, App
	26	14	77.8	1089	4	US-09-891-641-30	Sequence 30, Appl
	27	14	77.8	2195	4	US-09-949-016-677	Sequence 677, App
	28	14	77.8	2195	4	US-09-949-016-2715	Sequence 2715, Ap
	29	14	77.8	60095	4	US-09-949-016-12419	Sequence 12419, A
	30	14	77.8	60095	4	US-09-949-016-14457	Sequence 14457, A
	31	13.8	76.7	288	4	US-09-270-767-26956	Sequence 26956, A
	32	13.8	76.7	423	4	US-09-463-239-1	Sequence 1, Appli
c	33	13.8	76.7	601	4	US-09-949-016-82180	Sequence 82180, A
c	34	13.8	76.7	601	4	US-09-949-016-82181	Sequence 82181, A
c	35	13.8	76.7	601	4	US-09-949-016-82182	Sequence 82182, A
c	36	13.8	76.7	601	4	US-09-949-016-205054	Sequence 205054,
c	37	13.8	76.7	601	4	US-09-949-016-205055	Sequence 205055,
c	38	13.8	76.7	601	4	US-09-949-016-205056	Sequence 205056,
	39	13.8	76.7	622	3	US-09-129-030-46	Sequence 46, Appl
	40	13.8	76.7	699	4	US-09-107-532A-1581	Sequence 1581, Ap
	41	13.8	76.7	929	4	US-09-270-767-13423	Sequence 13423, A
	42	13.8	76.7	1155	4	US-09-902-540-7881	Sequence 7881, Ap
	43	13.8	76.7	1392	4	US-09-489-039A-4664	Sequence 4664, Ap
c	44	13.8	76.7	1440	2	US-08-224-482-5	Sequence 5, Appli
	45	13.8	76.7	1470	4	US-09-902-540-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11868
; LENGTH: 300598
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(300598)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

Query Match 85.6%; Score 15.4; DB 4; Length 300598;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGG 17
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Db 218203 TGCATAGATGCAGGGGG 218187

RESULT 2
US-09-949-016-14588/c
; Sequence 14588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14588
;   LENGTH: 302604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(302604)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588

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  Best Local Similarity   94.1%;  Pred. No. 2.7e+02;
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Qy          1 TGCATCGATGCAGGGGG 17
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RESULT 3
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; Sequence 14589, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14589
;   LENGTH: 302604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(302604)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGG 17
              ||||| ||||||||||||
Db     268209 TGCATAGATGCAGGGGG 268193


RESULT 4
US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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; SEQ ID NO 17119
;   LENGTH: 308362
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(308362)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

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  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGG 17
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Db     268025 TGCATAGATGCAGGGGG 268009


RESULT 5
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
;  APPLICANT: BASBAUM, CAROL
;  APPLICANT: GALLUP, MARIANNE
;  APPLICANT: DAIZONG, LI
;  APPLICANT: GEBREMICHAEL, ASSEFA
;  APPLICANT: GENSCH, ERIN
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
;  TITLE OF INVENTION: GENE EXPRESSION
;  FILE REFERENCE: UCSF12/02
;  CURRENT APPLICATION NUMBER: US/09/248,571
;  CURRENT FILING DATE: 1999-02-11
;  EARLIER APPLICATION NUMBER: 60/074,398
;  EARLIER FILING DATE: 1998-02-11
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 3358
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-248-571-2

  Query Match             82.2%;  Score 14.8;  DB 3;  Length 3358;
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  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||| | ||||||||||||
Db        999 TGCACCCATGCAGGGGGG 1016


RESULT 6
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
;  APPLICANT:  BASBAUM, Carol
;  APPLICANT:  GALLUP, Marianne
;  APPLICANT:  DAIZONG, Li
;  APPLICANT:  GEBREMICHAEL, Assefa
;  APPLICANT:  GENSCH, Erin
```

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;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
;  TITLE OF INVENTION:  MUCIN GENE EXPRESSION
;  FILE REFERENCE:  UCSF-012/03US
;  CURRENT APPLICATION NUMBER: US/09/553,736
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER:  US 09/248,571
;  PRIOR FILING DATE:  1999-02-11
;  PRIOR APPLICATION NUMBER:  US 60/074,398
;  PRIOR FILING DATE:  1998-02-11
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3358
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-553-736-2

  Query Match             82.2%;  Score 14.8;  DB 3;  Length 3358;
  Best Local Similarity   88.9%;  Pred. No. 3.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||| | ||||||||||
Db        999 TGCACCCATGCAGGGGGG 1016


RESULT 7
US-09-949-016-12476/c
; Sequence 12476, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12476
;   LENGTH: 17032
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12476

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 17032;
  Best Local Similarity   88.9%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||||| ||||||||| |
Db       5049 TGCATCAATGCAGGGGAG 5032


RESULT 8
US-09-949-016-13352/c
; Sequence 13352, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13352
;   LENGTH: 17032
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13352

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 17032;
  Best Local Similarity   88.9%;  Pred. No. 4.2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              |||||| ||||||||| |
Db       5049 TGCATCAATGCAGGGGAG 5032


RESULT 9
US-09-949-016-15317
; Sequence 15317, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15317
;   LENGTH: 37004
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15317

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 37004;
  Best Local Similarity   88.9%;  Pred. No. 4.5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||| |||||||| |||
Db      13090 TGCATAGATGCAGGTGGG 13107


RESULT 10
US-09-949-016-11757/c
; Sequence 11757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11757
;   LENGTH: 131631
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(131631)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11757

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 131631;
  Best Local Similarity   88.9%;  Pred. No. 5e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||| |||||||| |||
Db     129056 TGCATGGATGCAGGAGGG 129039


RESULT 11
US-09-270-767-14521
; Sequence 14521, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14521
;   LENGTH: 736
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-14521

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 736;
  Best Local Similarity   93.8%;  Pred. No. 4.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGG 16
              |||||||||||||| |
Db        691 TGCATCGATGCAGGAG 706


RESULT 12
US-09-252-991A-13644/c
; Sequence 13644, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13644
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13644

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1086;
  Best Local Similarity   93.8%;  Pred. No. 5.1e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCATCGATGCAGGGGG 17
              |||||||||| |||||
Db        264 GCATCGATGCCGGGGG 249


RESULT 13
US-09-252-991A-13444/c
; Sequence 13444, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13444
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13444

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1092;
  Best Local Similarity   93.8%;  Pred. No. 5.1e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCATCGATGCAGGGGG 17
              |||||||||| |||||
Db        305 GCATCGATGCCGGGGG 290


RESULT 14
US-09-252-991A-13697
; Sequence 13697, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13697
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13697

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1194;
  Best Local Similarity   93.8%;  Pred. No. 5.1e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCATCGATGCAGGGGG 17
              |||||||||| |||||
Db        971 GCATCGATGCCGGGGG 986


RESULT 15
US-09-079-592-1/c
; Sequence 1, Application US/09079592B
; Patent No. 6664092
; GENERAL INFORMATION:
;  APPLICANT:  Alexander Blinkovsky
```

; APPLICANT: Kimberly Brown
; APPLICANT: Michael W. Rey
; APPLICANT: Alan Klotz
; APPLICANT: Tony Byun
; TITLE OF INVENTION: Polypeptides Having Dipeptidyl
; TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5254.200-US
; CURRENT APPLICATION NUMBER: US/09/079,592B
; CURRENT FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 08/857,884
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: 60/062,892
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4280
; TYPE: DNA
; ORGANISM: Aspergillus
US-09-079-592-1

Query Match 80.0%; Score 14.4; DB 4; Length 4280;
Best Local Similarity 93.8%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCATCGATGCAGGGG 16
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Db       3367 TGCATCGATCCAGGGG 3352
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Search completed: April 29, 2005, 12:02:38
Job time : 60.7872 secs

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 241.419 Seconds
(without alignments)
453.893 Million cell updates/sec

Title: US-10-068-160A-12
Perfect score: 18
Sequence: 1 tgcatcgatgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	11	US-09-874-991C-503	Sequence 503, App
2	18	100.0	18	11	US-09-874-991C-513	Sequence 513, App
3	18	100.0	18	11	US-09-874-991C-551	Sequence 551, App
4	18	100.0	18	14	US-10-068-160-12	Sequence 12, Appl
5	18	100.0	18	19	US-10-499-597-16	Sequence 16, Appl
6	18	100.0	20	11	US-09-874-991C-494	Sequence 494, App
7	18	100.0	20	11	US-09-874-991C-502	Sequence 502, App
8	18	100.0	20	11	US-09-874-991C-505	Sequence 505, App
9	18	100.0	20	11	US-09-874-991C-512	Sequence 512, App
10	18	100.0	20	11	US-09-874-991C-538	Sequence 538, App
11	18	100.0	20	11	US-09-874-991C-546	Sequence 546, App
12	18	100.0	20	11	US-09-874-991C-550	Sequence 550, App
13	18	100.0	20	14	US-10-068-160-1	Sequence 1, Appli
14	18	100.0	20	14	US-10-068-160-38	Sequence 38, Appl
15	18	100.0	20	14	US-10-068-160-54	Sequence 54, Appl
16	18	100.0	20	15	US-10-194-035-32	Sequence 32, Appl
17	18	100.0	20	15	US-10-194-035-34	Sequence 34, Appl
18	18	100.0	20	15	US-10-194-035-37	Sequence 37, Appl
19	18	100.0	20	15	US-10-194-035-38	Sequence 38, Appl
20	18	100.0	20	15	US-10-194-035-43	Sequence 43, Appl
21	18	100.0	20	15	US-10-194-035-72	Sequence 72, Appl
22	18	100.0	20	18	US-10-666-022-1	Sequence 1, Appli
23	18	100.0	20	18	US-10-666-022-176	Sequence 176, App
24	18	100.0	20	18	US-10-666-022-177	Sequence 177, App
25	18	100.0	20	18	US-10-730-776-6	Sequence 6, Appli
26	18	100.0	20	18	US-10-730-776-7	Sequence 7, Appli
27	18	100.0	20	18	US-10-486-755-1	Sequence 1, Appli
28	18	100.0	20	18	US-10-486-755-5	Sequence 5, Appli
29	18	100.0	20	18	US-10-486-755-15	Sequence 15, Appl
30	18	100.0	20	18	US-10-486-755-16	Sequence 16, Appl
31	18	100.0	20	18	US-10-486-755-22	Sequence 22, Appl
32	18	100.0	20	19	US-10-499-597-12	Sequence 12, Appl
33	18	100.0	20	19	US-10-499-597-24	Sequence 24, Appl
34	18	100.0	20	19	US-10-499-597-38	Sequence 38, Appl
35	18	100.0	20	19	US-10-865-245-70	Sequence 70, Appl
36	18	100.0	22	11	US-09-874-991C-500	Sequence 500, App
37	18	100.0	22	11	US-09-874-991C-544	Sequence 544, App
38	18	100.0	26	11	US-09-874-991C-524	Sequence 524, App
39	18	100.0	26	11	US-09-874-991C-536	Sequence 536, App
40	18	100.0	28	11	US-09-874-991C-515	Sequence 515, App
41	18	100.0	28	11	US-09-874-991C-523	Sequence 523, App
42	18	100.0	28	11	US-09-874-991C-527	Sequence 527, App
43	18	100.0	28	11	US-09-874-991C-535	Sequence 535, App
44	18	100.0	29	11	US-09-874-991C-533	Sequence 533, App
45	18	100.0	30	11	US-09-874-991C-521	Sequence 521, App

ALIGNMENTS

RESULT 1
US-09-874-991C-503
; Sequence 503, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-503

Query Match 100.0%; Score 18; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 1 TGCATCGATGCAGGGGGG 18

RESULT 2

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US-09-874-991C-513
; Sequence 513, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-513

  Query Match             100.0%;  Score 18;  DB 11;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          1 TGCATCGATGCAGGGGGG 18


RESULT 3
US-09-874-991C-551
; Sequence 551, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 551
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-551

  Query Match             100.0%;  Score 18;  DB 11;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          1 TGCATCGATGCAGGGGGG 18


RESULT 4
US-10-068-160-12
; Sequence 12, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-12

  Query Match             100.0%;  Score 18;  DB 14;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          1 TGCATCGATGCAGGGGGG 18


RESULT 5
US-10-499-597-16
; Sequence 16, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Rouse, Barry T.
;  APPLICANT:  Zheng, Mei
;  TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
;  FILE REFERENCE: 4239-64125-02
;  CURRENT APPLICATION NUMBER: US/10/499,597
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: PCT/US02/40955
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,457
;  PRIOR FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG D oligonucleotide
US-10-499-597-16

  Query Match             100.0%;  Score 18;  DB 19;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          1 TGCATCGATGCAGGGGGG 18


RESULT 6
US-09-874-991C-494
; Sequence 494, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
```

; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-494

Query Match 100.0%; Score 18; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 7
US-09-874-991C-502
; Sequence 502, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 502
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-502

Query Match 100.0%; Score 18; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 8
US-09-874-991C-505
; Sequence 505, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 505
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-505

Query Match 100.0%; Score 18; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 9
US-09-874-991C-512
; Sequence 512, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 512
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-512

Query Match 100.0%; Score 18; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGATGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCATCGATGCAGGGGGG 20

RESULT 10
US-09-874-991C-538
; Sequence 538, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-538

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  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20


RESULT 11
US-09-874-991C-546
; Sequence 546, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 546
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-546

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 12
US-09-874-991C-550
; Sequence 550, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 550
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-550

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCATCGATGCAGGGGGG 20


RESULT 13
US-10-068-160-1
; Sequence 1, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-1

  Query Match             100.0%;  Score 18;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 18;
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Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20


RESULT 14
US-10-068-160-38
; Sequence 38, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-38

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  Best Local Similarity   100.0%;  Pred. No. 18;
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Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20
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RESULT 15
US-10-068-160-54
; Sequence 54, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-54

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  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCATCGATGCAGGGGGG 18
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Db          3 TGCATCGATGCAGGGGGG 20


Search completed: April 29, 2005, 12:35:40
Job time : 241.419 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 712.216 Seconds
(without alignments)
1224.620 Million cell updates/sec

Title: US-10-068-160A-13
Perfect score: 18
Sequence: 1 tgcaccggtgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	20	6	AX194442	AX194442 Sequence
2	18	100.0	20	6	AX352200	AX352200 Sequence
3	18	100.0	20	6	AX352208	AX352208 Sequence
4	18	100.0	20	6	AX352211	AX352211 Sequence
5	18	100.0	20	6	AX352218	AX352218 Sequence
6	18	100.0	20	6	AX352244	AX352244 Sequence
7	18	100.0	20	6	AX465392	AX465392 Sequence
8	18	100.0	28	6	AX352221	AX352221 Sequence
9	18	100.0	28	6	AX352229	AX352229 Sequence
10	18	100.0	28	6	AX352233	AX352233 Sequence
11	18	100.0	28	6	AX352241	AX352241 Sequence
12	18	100.0	40	6	AX352252	AX352252 Sequence
13	17	94.4	10782	1	AE001002	AE001002 Archaeogl
14	16.4	91.1	20	6	AX194501	AX194501 Sequence
15	16.4	91.1	20	6	AX352199	AX352199 Sequence
16	16.4	91.1	20	6	AX352203	AX352203 Sequence
17	16.4	91.1	20	6	AX352210	AX352210 Sequence
18	16.4	91.1	20	6	AX352214	AX352214 Sequence
19	16.4	91.1	20	6	AX352247	AX352247 Sequence
20	16.4	91.1	28	6	AX352220	AX352220 Sequence
21	16.4	91.1	28	6	AX352224	AX352224 Sequence
22	16.4	91.1	28	6	AX352232	AX352232 Sequence
23	16.4	91.1	28	6	AX352236	AX352236 Sequence
24	16.4	91.1	124270	10	AC091518	AC091518 Mus muscu
c 25	16.4	91.1	155724	4	AC091316	AC091316 Sus scrof
c 26	16.4	91.1	201320	2	AC073816	AC073816 Mus muscu
27	16.4	91.1	202864	2	AC147644	AC147644 Gallus ga
28	16.4	91.1	204120	8	AY661659	AY661659 Sorghum b
29	16.4	91.1	233804	10	AC130831	AC130831 Mus muscu
c 30	16.4	91.1	240647	10	AC131745	AC131745 Mus muscu
c 31	16.4	91.1	300349	1	AE017319	AE017319 Desulfovi
c 32	16.4	91.1	347365	1	BX569691	BX569691 Synechoco
33	16	88.9	13787	1	AE013603	AE013603 Yersinia
34	16	88.9	47225	2	AC099869	AC099869 Mus muscu
c 35	16	88.9	110000	1	BX936398_43	Continuation (44 o
36	16	88.9	110000	2	AC105643_4	Continuation (5 of
37	16	88.9	210477	2	AC116555	AC116555 Mus muscu
c 38	16	88.9	235050	1	AJ414158	AJ414158 Yersinia
c 39	16	88.9	240918	2	AC137254	AC137254 Rattus no
40	16	88.9	264464	2	AC107410	AC107410 Rattus no
c 41	16	88.9	290924	1	AE017138	AE017138 Yersinia
42	16	88.9	323991	2	AC098512	AC098512 Rattus no
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45	15.4	85.6	342	11	AU027239	AU027239 Rattus no

ALIGNMENTS

RESULT 1
AX194442
LOCUS AX194442 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 42 from Patent WO0151500.
ACCESSION AX194442
VERSION AX194442.1 GI:15385098
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 42 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGGG 18
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Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 2
AX352200
LOCUS AX352200 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 496 from Patent WO0193902.
ACCESSION AX352200
VERSION AX352200.1 GI:18617483
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 496 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 3
AX352208
LOCUS       AX352208                20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 504 from Patent WO0193902.
ACCESSION   AX352208
VERSION     AX352208.1  GI:18617491
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 504 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 4
AX352211
LOCUS       AX352211                20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 507 from Patent WO0193902.
ACCESSION   AX352211
VERSION     AX352211.1  GI:18617494
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 507 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
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ORIGIN

  Query Match            100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 5
AX352218
LOCUS       AX352218                20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 514 from Patent WO0193902.
ACCESSION   AX352218
VERSION     AX352218.1  GI:18617501
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 514 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 6
AX352244
LOCUS       AX352244                20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 540 from Patent WO0193902.
ACCESSION   AX352244
VERSION     AX352244.1  GI:18617527
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 540 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
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Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 7
AX465392
LOCUS       AX465392                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 60 from Patent WO0211761.
ACCESSION   AX465392
VERSION     AX465392.1  GI:21899755
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 60 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 8
AX352221
LOCUS       AX352221                  28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 517 from Patent WO0193902.
ACCESSION   AX352221
VERSION     AX352221.1  GI:18617504
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 517 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
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ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 9
AX352229
LOCUS       AX352229                  28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 525 from Patent WO0193902.
ACCESSION   AX352229
VERSION     AX352229.1  GI:18617512
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 525 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 10
AX352233
LOCUS       AX352233                  28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 529 from Patent WO0193902.
ACCESSION   AX352233
VERSION     AX352233.1  GI:18617516
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 529 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
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Qy          1 TGCACCGGTGCAGGGGGG 18
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Db         11 TGCACCGGTGCAGGGGGG 28


RESULT 11
AX352241
LOCUS       AX352241                  28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 537 from Patent WO0193902.
ACCESSION   AX352241
VERSION     AX352241.1  GI:18617524
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
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  JOURNAL   Patent: WO 0193902-A 537 13-DEC-2001;
            Biosynexus Incorporated (US)
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db         11 TGCACCGGTGCAGGGGGG 28


RESULT 12
AX352252
LOCUS       AX352252                  40 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 548 from Patent WO0193902.
ACCESSION   AX352252
VERSION     AX352252.1  GI:18617535
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 548 13-DEC-2001;
            Biosynexus Incorporated (US)
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                     /note="Synthetic HDR"
ORIGIN

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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
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Db         16 TGCACCGGTGCAGGGGGG 33


RESULT 13
AE001002
LOCUS       AE001002               10782 bp    DNA     linear   BCT 17-MAR-2003
DEFINITION  Archaeoglobus fulgidus DSM 4304 section 105 of 172 of the complete
            genome.
ACCESSION   AE001002 AE000782
VERSION     AE001002.1  GI:2689325
KEYWORDS    .
SOURCE      Archaeoglobus fulgidus DSM 4304
  ORGANISM  Archaeoglobus fulgidus DSM 4304
            Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
            Archaeoglobaceae; Archaeoglobus.
REFERENCE   1  (bases 1 to 10782)
  AUTHORS   Klenk,H.P., Clayton,R.A., Tomb,J., White,O., Nelson,K.E.,
            Ketchum,K.A., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,
            Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyrpides,N.C.,
            Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill,S.,
            Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,
            Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A.,
            Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L.,
            Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
            Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C.,
            Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
            Woese,C.R. and Venter,J.C.
  TITLE     The complete genome sequence of the hyperthermophilic,
            sulphate-reducing archaeon Archaeoglobus fulgidus
  JOURNAL   Nature 390 (6658), 364-370 (1997)
  MEDLINE   98049343
   PUBMED   9389475
REFERENCE   2  (bases 1 to 10782)
  AUTHORS   Klenk,H.P., Clayton,R.A., Tomb,J.-F., White,O., Nelson,K.E.,
            Ketchum,K.A., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,
            Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyrpides,N.C.,
            Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill,S.,
            Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,
            Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A.,
            Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L.,
            Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
            Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C.,
            Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
            Woese,C.R. and Venter,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-1997) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
  REMARK    In order to show the genes in ascending order on the genome, the
            origin of this version has been moved by TIGR to position 2093570
            of the original version and the opposite strand is shown from the
            original version.
COMMENT     On Dec 16, 1997 this sequence version replaced gi:2649104.
FEATURES             Location/Qualifiers
     source          1. .10782
                     /organism="Archaeoglobus fulgidus DSM 4304"
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     gene            complement(159. .1019)
                     /gene="AF1454"
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                     putative"
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                     /db_xref="GI:2649115"
                     /translation="MKFRTLFNLLTACILLFADVRADTFQVDYKIYESNQGCGGKSKY
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                     PESGNIYLKISSGKEEQKYLFPFALQGATTITATASQAPATSHQVDLATQINSAVYSL
                     YIQLGLRKFIPYEHFRVVLILVPILIVAISYWVKKRSKKRLIEVEGVEIEGPYKKSIT
                     KLFANCHKCGKREYLPYQCNYCGNYFCGEHILPPKHDCPGEKEWRSKAPLPPGVVWEY
                     RSDGTTYRKY"
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     CDS             complement(2144. .2317)
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                     /db_xref="GI:2649116"
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                     /gene="tRNA-Cys-1"
     tRNA            complement(2652. .2723)
                     /gene="tRNA-Cys-1"
                     /product="tRNA-Cys"
                     /note="codon recognized: UGC"
     gene            complement(2811. .3128)
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                     /translation="MDARDIVLSVISVFSAAALVYRWLSLYDRVDMTVIFFATLLIAS
                     LTLLLISIELRMQRIMDEFKSVKRTIAVNSDDLEGRIERLFIEKVRDLEDKLESIERR
                     MYR"
     gene            3219. .5444
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     CDS             3219. .5444
                     /gene="AF1458"
                     /note="similar to GB:L77117 PID:1592139 percent identity:
                     48.13; identified by sequence similarity; putative"
                     /codon_start=1
                     /transl_table=11
                     /product="ATP-dependent RNA helicase, putative"
                     /protein_id="AAB89786.1"
                     /db_xref="GI:2649107"
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                     WEKARIVVSTPQVVENDLLAGRISLEDVILVVFDEAHRAVGNYAYVFIAKEYLRTAKK
                     PLILAMTASPGSDPERIMEVIQNLGIEAIEVRTEWDSDVAPYVGKKRIEWIKVDIPEE
                     MKEVKERLKECIKIRFKRLRELWIEVPENSSKRDLLALQEALQAEAASSQSSEIFEAL
                     SILAEIMKLQHAVELIETQGVKAVKSYLRKLVREATSKGGSKAAKSIVGDPIFKKAVI
                     ALSKCKVEHPKLEKLKEILKEQFEKNPDSRVIVFTNYRDSAEMLVNELSPLFPVAKFV
                     GQASRDNDKGMRQKEQIETIDKFRRGVYKVLVATSVGEEGLDIPSTDLVVFYEAVPSE
                     IRAIQRKGRTGRGREGRIVVLVTKGTRDEAYYYSSMKKERKMYDKILEIKRIIDRKQR
                     SIGDYVLPEETGIKVIVDSRELRSEVVKHLREIGAKIEIRNLEVADYVVSDRVAVERK
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                     FGIPVLRSSNARETAELIFAMARREQEERKRGVVEHTAKTKRTLKDEQEYIVSAISNV
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                     F"
     gene            5471. .5543
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                     /gene="tRNA-Thr-1"
                     /product="tRNA-Thr"
                     /note="codon recognized: ACC"
     gene            complement(5605. .5877)
                     /gene="AF1459"
     CDS             complement(5605. .5877)
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                     /note="similar to GB:L77117 SP:Q57735 PID:1499069 percent
                     identity: 35.38; identified by sequence similarity;
                     putative"
                     /codon_start=1
                     /transl_table=11
                     /product="conserved hypothetical protein"
                     /protein_id="AAB89785.1"
                     /db_xref="GI:2649106"
                     /translation="MTRRDRLEIIYDILSIIRKHGNSILPTPLLRFSNLSTQNFNRYM
                     DELVKKGLVREIQDESGRRYYSLTDKGFRFLEKYQKIREFIEEFGL"
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                     /codon_start=1
                     /transl_table=11
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                     /db_xref="GI:2649112"
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                     SAAILYTIYSLLWRWLERFPGEVVINGVALVIALTSLLSRMPLVFLISQLALVFLLVA
                     AIFVNYSHFRHESRSKRAYPLYILLFVFWLLNISLTFRFLPLEFRFAIYTLSVAVILI
                     IAYRVLRKL"
     gene            6658. .6891
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                     /codon_start=1
                     /transl_table=11
                     /product="iron-sulfur cluster binding protein, putative"
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                     /db_xref="GI:2649108"
                     /translation="MRLGGDSEVVVEQISGCIGCGTCVEVCPTDVFRLEGGRAVIKYP
                     EDCQICHLCRLYCPVDAITISPEKSLPVIVAWG"
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                     putative"
                     /codon_start=1
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                     /protein_id="AAB89790.1"
                     /db_xref="GI:2649111"

  Query Match             94.4%;  Score 17;  DB 1;  Length 10782;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGG 17
              |||||||||||||||||
Db       8164 TGCACCGGTGCAGGGGG 8180


RESULT 14
AX194501
LOCUS       AX194501                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 101 from Patent WO0151500.
ACCESSION   AX194501
VERSION     AX194501.1  GI:15385157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 101 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGG 18
              ||||||| ||||||||||
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Db          3 TGCACCGATGCAGGGGGG 20


RESULT 15
AX352199
LOCUS       AX352199                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 495 from Patent WO0193902.
ACCESSION   AX352199
VERSION     AX352199.1  GI:18617482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 495 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||| ||||||||||||
Db          3 TGCAGCGGTGCAGGGGGG 20


Search completed: April 29, 2005, 08:03:45
Job time : 715.341 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 183.527 Seconds
(without alignments)
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Title: US-10-068-160A-13
Perfect score: 18
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	20	4	AAC80622	Aac80622 Immunogen
2	18	100.0	20	4	AAS09592	Aas09592 Immunorea
3	18	100.0	20	6	ABL35614	Abl35614 Immunosti
4	18	100.0	20	6	ABL35578	Abl35578 Immunosti
5	18	100.0	20	6	ABL35581	Abl35581 Immunosti
6	18	100.0	20	6	ABL35570	Abl35570 Immunosti
7	18	100.0	20	6	ABL35588	Abl35588 Immunosti
8	18	100.0	20	6	ABK46470	Abk46470 Immunosti
9	18	100.0	20	8	ACC48296	Acc48296 CpG oligo
10	18	100.0	20	8	ACC48300	Acc48300 CpG oligo
11	18	100.0	20	8	ACC48313	Acc48313 CpG oligo
12	18	100.0	20	9	ACC83118	Acc83118 D class C
13	18	100.0	20	9	ACC83152	Acc83152 D class O
14	18	100.0	20	10	ADD01049	Add01049 CpG D oli
15	18	100.0	20	12	ADN96868	Adn96868 Immunosti
16	18	100.0	20	12	ADN97044	Adn97044 Immunosti
17	18	100.0	28	6	ABL35599	Abl35599 Immunosti
18	18	100.0	28	6	ABL35603	Abl35603 Immunosti
19	18	100.0	28	6	ABL35591	Abl35591 Immunosti
20	18	100.0	28	6	ABL35611	Abl35611 Immunosti
21	18	100.0	40	6	ABL35622	Abl35622 Immunosti
22	16.4	91.1	20	4	AAS09651	Aas09651 Immunorea
23	16.4	91.1	20	6	ABL35573	Abl35573 Immunosti
24	16.4	91.1	20	6	ABL35584	Abl35584 Immunosti
25	16.4	91.1	20	6	ABL35569	Abl35569 Immunosti
26	16.4	91.1	20	6	ABL35617	Abl35617 Immunosti
27	16.4	91.1	20	6	ABL35580	Abl35580 Immunosti
28	16.4	91.1	20	8	ACC48311	Acc48311 CpG oligo
29	16.4	91.1	20	8	ACC48320	Acc48320 CpG oligo
30	16.4	91.1	20	8	ACC48321	Acc48321 CpG oligo
31	16.4	91.1	20	9	ACC83125	Acc83125 D class C
32	16.4	91.1	20	9	ACC83116	Acc83116 D class C
33	16.4	91.1	20	9	ACC83126	Acc83126 D class C
34	16.4	91.1	20	10	ADD01076	Add01076 CpG D oli
35	16.4	91.1	20	10	ADD01059	Add01059 CpG D oli
36	16.4	91.1	28	6	ABL35590	Abl35590 Immunosti
37	16.4	91.1	28	6	ABL35594	Abl35594 Immunosti
38	16.4	91.1	28	6	ABL35606	Abl35606 Immunosti
39	16.4	91.1	28	6	ABL35602	Abl35602 Immunosti
40	15.4	85.6	19	4	AAC80602	Aac80602 Immunogen
41	15.4	85.6	19	4	AAS09572	Aas09572 Immunorea
42	15.4	85.6	19	6	ABK46450	Abk46450 Immunosti
c 43	15.4	85.6	278	5	ABA12385	Aba12385 Human ner
c 44	15.4	85.6	349	4	AAL01438	Aal01438 Human rep
c 45	15.4	85.6	349	4	ABL96885	Abl96885 Human tes

ALIGNMENTS

RESULT 1
AAC80622
ID AAC80622 standard; DNA; 20 BP.
XX
AC AAC80622;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX

PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 2
AAS09592
ID AAS09592 standard; DNA; 20 BP.
XX
AC AAS09592;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #42.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 34; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 3
ABL35614
ID ABL35614 standard; DNA; 20 BP.
XX
AC ABL35614;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 540.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.

```
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 62; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 4
ABL35578
ID   ABL35578 standard; DNA; 20 BP.
XX
AC   ABL35578;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 504.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

```
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 5
ABL35581
ID   ABL35581 standard; DNA; 20 BP.
XX
AC   ABL35581;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 507.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
```

```
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 6
ABL35570
ID   ABL35570 standard; DNA; 20 BP.
XX
AC   ABL35570;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 496.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 7
ABL35588
ID   ABL35588 standard; DNA; 20 BP.
XX
AC   ABL35588;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 514.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .20
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
```

```
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 61; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 8
ABK46470
ID   ABK46470 standard; DNA; 20 BP.
XX
AC   ABK46470;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Immunostimulatory unmethylated CpG oligodideoxynucleotide #60.
XX
KW   unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW   Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW   viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW   bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS   Synthetic.
XX
PN   WO200211761-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US041633.
XX
PR   10-AUG-2000; 2000US-0224011P.
PR   01-SEP-2000; 2000US-0229307P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Mond JJ,  Prince G,  Klinman DM;
XX
DR   WPI; 2002-227118/28.
XX
PT   Vaccine for immunizing patient against respiratory syncytial virus, has
PT   epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT   linked by phosphate bond-oligodideoxynucleotides.
XX
PS   Claim 4; Page 8; 30pp; English.
XX
CC   The invention describes a vaccine comprising one or more epitopes of a
CC   Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC   guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC   vaccine is useful for vaccinating a patient especially against viruses of
CC   the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC   primary cause of viral bronchiolitis and pneumonia in infants and
CC   children, and infectious pulmonary disease in infants. RSV has been
CC   particularly implicated in death of infants that are premature, have
CC   bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC   represents an oligodideoxynucleotide that can be used in the creation of
CC   the vaccine
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 9
ACC48296
ID   ACC48296 standard; DNA; 20 BP.
XX
AC   ACC48296;
XX
DT   11-AUG-2003  (first entry)
XX
DE   CpG oligodeoxynucleotide D29 used for dendritic cell maturation.
XX
KW   CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW   cytostatic; immunostimulant; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate nucleotides"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate nucleotide"
XX
PN   WO2003020884-A2.
XX
PD   13-MAR-2003.
XX
PF   13-AUG-2002; 2002WO-US025732.
XX
PR   14-AUG-2001; 2001US-0312190P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel M,  Verthelyi D;
XX
DR   WPI; 2003-300874/29.
XX
```

```
PT   Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT   for activating the immune system to treat diseases such as cancer,
PT   comprises contacting a dendritic cell precursor with a D type
PT   oligodeoxynucleotide.
XX
PS   Claim 11; Page 44; 69pp; English.
XX
CC   The present sequence is that of D type CpG oligodeoxynucleotide D29,
CC   which is used in a claimed method for generating a mature dendritic cell.
CC   The method involves contacting a dendritic cell precursor, especially a
CC   monocyte, with the oligonucleotide. The method is useful for generating
CC   mature dendritic cells and enhancing T cell responses, thus enhancing
CC   antigen presentation. Mature dendritic cells are useful for tumour
CC   immunotherapy, for augmenting an immune response to an infectious agent
CC   or to a vaccine, and as vaccines to prevent future infection or to
CC   activate the immune system to treat diseases such as cancer. Mature
CC   dendritic cells may also be used to produce activated T lymphocytes
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 10
ACC48300
ID   ACC48300 standard; DNA; 20 BP.
XX
AC   ACC48300;
XX
DT   11-AUG-2003  (first entry)
XX
DE   CpG oligodeoxynucleotide used for dendritic cell maturation.
XX
KW   CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW   cytostatic; immunostimulant; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "N is any base (especially G) or no base"
FT   misc_difference 2
FT                   /*tag=  b
FT                   /note= "N is any base (especially G) or no base"
XX
PN   WO2003020884-A2.
XX
PD   13-MAR-2003.
XX
PF   13-AUG-2002; 2002WO-US025732.
XX
PR   14-AUG-2001; 2001US-0312190P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel M,  Verthelyi D;
XX
DR   WPI; 2003-300874/29.
XX
PT   Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT   for activating the immune system to treat diseases such as cancer,
PT   comprises contacting a dendritic cell precursor with a D type
PT   oligodeoxynucleotide.
XX
PS   Disclosure; Page 26; 69pp; English.
XX
CC   The present sequence is that of a D type CpG oligodeoxynucleotide that is
CC   an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
CC   invention. Mature dendritic cells are obtained by contacting a dendritic
CC   cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
CC   The method is useful for generating mature dendritic cells and enhancing
CC   T cell responses, thus enhancing antigen presentation. Mature dendritic
CC   cells are useful for tumour immunotherapy, for augmenting an immune
CC   response to an infectious agent or to a vaccine, and as vaccines to
CC   prevent future infection or to activate the immune system to treat
CC   diseases such as cancer. Mature dendritic cells may also be used to
CC   produce activated T lymphocytes
XX
SQ   Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;

  Query Match             100.0%;  Score 18;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 11
ACC48313
ID   ACC48313 standard; DNA; 20 BP.
XX
AC   ACC48313;
XX
DT   11-AUG-2003  (first entry)
XX
DE   CpG oligodeoxynucleotide.
XX
KW   CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW   cytostatic; immunostimulant; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   WO2003020884-A2.
XX
PD   13-MAR-2003.
XX
PF   13-AUG-2002; 2002WO-US025732.
XX
PR   14-AUG-2001; 2001US-0312190P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel M,  Verthelyi D;
XX
DR   WPI; 2003-300874/29.
XX
PT   Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT   for activating the immune system to treat diseases such as cancer,
PT   comprises contacting a dendritic cell precursor with a D type
PT   oligodeoxynucleotide.
XX
PS   Disclosure; Page 61; 69pp; English.
XX
CC   The present sequence is that of a CpG oligodeoxynucleotide of the
CC   invention. A claimed method for generating dendritic cells involves
CC   contacting a dendritic cell precursor, especially a monocyte, with a D
CC   type oligodeoxynucleotide (see ACC48294) containing a central
CC   unmethylated CpG motif. The method is useful for generating mature
CC   dendritic cells and enhancing T cell responses, thus enhancing antigen
CC   presentation. Mature dendritic cells are useful for tumour immunotherapy,
CC   for augmenting an immune response to an infectious agent or to a vaccine,
CC   and as vaccines to prevent future infection or to activate the immune
CC   system to treat diseases such as cancer. Mature dendritic cells may also
CC   be used to produce activated T lymphocytes
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
```

```
  Query Match             100.0%;  Score 18;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20
```

RESULT 12
ACC83118
ID ACC83118 standard; DNA; 20 BP.
XX
AC ACC83118;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.
XX
OS Unidentified.
XX
PN WO2003040308-A2.
XX
PD 15-MAY-2003.
XX
PF 29-JUL-2002; 2002WO-US024235.
XX
PR 27-JUL-2001; 2001US-0308283P.
PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10C; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 18;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20
```

RESULT 13
ACC83152
ID ACC83152 standard; DNA; 20 BP.
XX
AC ACC83152;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class ODN sequence useful for encapsulating in SSCL, D29.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; phosphorothioate backbone; ss.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT modified_base   16. .20
FT   /*tag= a
FT   /mod_base= OTHER
FT   /note= "Phosphorothioate backbone"
XX
PN WO2003040308-A2.
XX
PD 15-MAY-2003.
XX
PF 29-JUL-2002; 2002WO-US024235.
XX
PR 27-JUL-2001; 2001US-0308283P.
PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Example 8; Page 52; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class ODN

CC potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 14
ADD01049
ID ADD01049 standard; DNA; 20 BP.
XX
AC ADD01049;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG D oligonucleotide SEQ ID NO:13.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerary; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
PN WO2003054161-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Zheng M, Rouse BT;
XX
DR WPI; 2003-559138/52.
XX
PT Inducing the production of vascular endothelial growth factor by a cell,
PT useful for inducing angiogenesis, comprises contacting the cell with a
PT CpG oligodeoxynucleotide.
XX
PS Example 7; SEQ ID NO 13; 37pp; English.
XX
CC The present invention describes a method for inducing the production of
CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC the cell with a CpG oligonucleotide and therefore inducing the production
CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC tissue, comprising introducing a CpG oligonucleotide into an area of the
CC tissue where the formation of new blood vessels is desired, and so
CC inducing neovascularisation in the area of the tissue; (2) promoting
CC angiogenesis in an area of the subject where angiogenesis is desired,
CC comprising introducing a CpG oligonucleotide to the area, and so
CC promoting angiogenesis in the subject; and (3) screening for an agent
CC that inhibits neovascularisation, comprising administering a CpG
CC oligonucleotide to a non-human mammal and administering the agent to the
CC mammal, where inhibition of angiogenesis in the animal indicates that the
CC agent is effective in inhibiting neovascularisation. The CpG
CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC activities, and can be used in gene therapy. The method and the CpG
CC oligonucleotides can be used in inducing angiogenesis or
CC neovascularisation, such as in subjects with a skin graft, subjects who
CC exhibit male pattern baldness, or subjects who have a wound or who have
CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a CpG oligonucleotide which is used in the exemplification of
CC the present invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 15
ADN96868
ID ADN96868 standard; DNA; 20 BP.
XX
AC ADN96868;
XX
DT 26-AUG-2004 (first entry)
XX
DE Immunostimulatory D CpG oligonucleotide seqid 2.
XX
KW virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;
KW tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;
KW dermatological; bacterial growth inhibitor; immunostimulator;
KW immune response; immunostimulatory; opportunistic infection;
KW lentivirus infection; human immunodeficiency virus infection; AIDS;
KW Leishmania infection; bacterial infection; fungal infection;
KW viral infection; protozoan infection; prion disease; nucleoplasm;
KW salmonellosis; syphilis; neurosyphilis; tuberculosis;
KW bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;
KW cryptococcal meningitis; hepatitis B; histoplasmosis; cryptosporidiosis;
KW isosporiasis; microsporidiosis; pneumocystis carinii pneumonia;
KW toxoplasmosis; cytomegalovirus; hepatitis; herpes simplex; herpes zoster;
KW human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;
KW progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;
KW systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;
KW HSV; genital herpes; HZV; shingles; genital wart; cervical cancer;
KW immunostimulatory CpG oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004105872-A1.
XX
PD 03-JUN-2004.
XX
PF 17-SEP-2003; 2003US-00666022.
XX
PR 18-SEP-2002; 2002US-0411944P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Verthelyi D;
XX
DR WPI; 2004-419442/39.
XX
PT Increasing an immune response to an opportunistic infection e.g.
PT bacterial infections in an immunocompromised subject involves
PT administering immunostimulatory D oligodeoxynucleotide or an
PT immunostimulatory K oligodeoxynucleotide.
XX
PS Claim 21; SEQ ID NO 2; 64pp; English.
XX
CC The invention describes a method of increasing an immune response to an
CC opportunistic infection in an immunocompromised subject involves
CC administering an immunostimulatory D oligodeoxynucleotide or an
CC immunostimulatory K oligodeoxynucleotide, where an antigenic epitope of a
CC polypeptide is not administered to the subject. The method is useful for
CC increasing an immune response to an opportunistic infection e.g.
CC infection with a lentivirus such as human immunodeficiency virus
CC (including HIV-1, HIV-2) e.g. AIDS; infection with Leishmania; bacterial
CC infections; fungal infections; viral infections; protozoan infections;

CC prion disease; and nucleoplasm in an immunocompromised subject or a
CC subject infected with a lentivirus. The bacterial infections include
CC salmonellosis, syphilis and neurosyphilis, tuberculosis and bacillary
CC angiomatosis, the fungal infections include aspergillosis, candidiasis,
CC coccidioidomycosis, cryptococcal meningitis, hepatitis B, and
CC histoplasmosis, the protozoal infections include cryptosporidiosis,
CC isosporiasis, microsporidiosis, pneumocystis carinii pneumonia and
CC toxoplasmosis, viral infections include cytomegalovirus, hepatitis,
CC herpes simplex, herpes zoster, human papilloma virus, molluscum
CC contagiosum, oral hairy leukoplakia and progressive multifocal
CC leukoencephalopathy and neoplasms include Kaposi's sarcoma, systemic non-
CC Hodgkin's lymphoma and primary central nervous system lymphoma. The
CC herpes simplex includes HSV, genital herpes. The herpes zoster includes
CC HZV and shingles. The human papilloma virus includes HPV, genital warts
CC and cervical cancer. The method stimulates immune responses to any
CC opportunistic infection in immunocompromised subjects. This sequence
CC represents an immunostimulatory CpG oligonucleotide sequence that
CC stimulate the release of cytokines from cells of the immune system and
CC can be used to increase immune response in the method of the invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20
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Job time : 183.527 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1687.62 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-13
Perfect score: 18
Sequence: 1 tgcaccggtgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	94.4	594	7	CO665888	CO665888 DG33-105o
	2	17	94.4	840	9	CG271799	CG271799 OG0DZ26TV
c	3	16.4	91.1	54	9	CR086950	CR086950 Reverse s
c	4	16.4	91.1	245	2	AW325275	AW325275 TENU4637
c	5	16.4	91.1	277	8	AQ444154	AQ444154 GSSTc0207
c	6	16.4	91.1	339	6	CB076094	CB076094 hf37c06.g
c	7	16.4	91.1	440	6	CB087291	CB087291 hj98g11.g
c	8	16.4	91.1	509	6	CB087214	CB087214 hj97e04.g
	9	16.4	91.1	562	1	AI370313	AI370313 qv76e01.x
c	10	16.4	91.1	598	6	CB087525	CB087525 hk03f05.g
	11	16.4	91.1	610	9	CG692380	CG692380 ZMMBBb029
c	12	16.4	91.1	665	7	CN788545	CN788545 4122892 B
c	13	16.4	91.1	684	4	BM624520	BM624520 170006874
c	14	16.4	91.1	692	4	BM620160	BM620160 170006874
c	15	16.4	91.1	708	4	BM621890	BM621890 170006874
c	16	16.4	91.1	779	8	CC109078	CC109078 NDL.50B23
c	17	16.4	91.1	799	8	CC133230	CC133230 NDL.50B22
c	18	16.4	91.1	866	7	CK151795	CK151795 FGAS03452
	19	16.4	91.1	921	9	CL509000	CL509000 SAIL_807_
	20	16.4	91.1	1005	9	CNS040Z1	AL269542 Tetraodon
c	21	16.4	91.1	1120	8	CC214014	CC214014 CH261-3F1
c	22	16.4	91.1	1200	6	CD256849	CD256849 AGENCOURT
	23	16	88.9	553	6	CB334319	CB334319 3529_1_24
c	24	16	88.9	700	4	BI897515	BI897515 fm62g02.y
c	25	16	88.9	969	9	CNS03H3D	AL243778 Tetraodon
	26	16	88.9	982	9	CNS042UH	AL271970 Tetraodon
	27	16	88.9	1157	5	BX426076	BX426076 BX426076
	28	16	88.9	1309	4	BM559504	BM559504 AGENCOURT
c	29	15.4	85.6	105	6	CB486533	CB486533 omyktpt10
c	30	15.4	85.6	160	6	CB016628	CB016628 pgn1c.pk0
	31	15.4	85.6	165	9	CL979165	CL979165 OsIFCC032
c	32	15.4	85.6	220	9	CC622603	CC622603 OGUKS09TV
	33	15.4	85.6	253	2	BE148995	BE148995 CM0-HT024
c	34	15.4	85.6	274	1	AV108043	AV108043 AV108043
c	35	15.4	85.6	331	1	AI216300	AI216300 qg76c11.x
c	36	15.4	85.6	331	5	BX268033	BX268033 BX268033
	37	15.4	85.6	332	6	CB406325	CB406325 OSTR070G1
c	38	15.4	85.6	344	8	AQ067086	AQ067086 HS_2233_A
	39	15.4	85.6	375	5	BY315784	BY315784 BY315784
c	40	15.4	85.6	391	6	CD598131	CD598131 RK112A1D0
c	41	15.4	85.6	397	9	CE437108	CE437108 tigr-gss-
	42	15.4	85.6	402	9	CE182406	CE182406 tigr-gss-
c	43	15.4	85.6	405	4	BM487257	BM487257 pgm2n.pk0
c	44	15.4	85.6	408	1	AI146003	AI146003 UI-R-BT0-
c	45	15.4	85.6	411	2	BF386534	BF386534 UI-R-CA1-

ALIGNMENTS

RESULT 1
CO665888
LOCUS CO665888 594 bp mRNA linear EST 26-JUL-2004
DEFINITION DG33-105o6 DG33-aorta Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO665888
VERSION CO665888.1 GI:50605135
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 594)
AUTHORS Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H., Henrich,J. and Loebbert,R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
FEATURES Location/Qualifiers
source 1. .594
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="aorta"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG33-aorta"
/note="Organ: aorta; Vector: Dog pBluescript LION"
ORIGIN

Query Match 94.4%; Score 17; DB 7; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGGGGG 18
||||||||||||||||||
Db 536 GCACCGGTGCAGGGGGG 552

RESULT 2
CG271799
LOCUS CG271799 840 bp DNA linear GSS 25-AUG-2003

```
DEFINITION  OG0DZ26TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0696F04,
            genomic survey sequence.
ACCESSION   CG271799
VERSION     CG271799.1  GI:34183940
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG0DZ26TH
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0696F04"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             94.4%;  Score 17;  DB 9;  Length 840;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCACCGGTGCAGGGGGG 18
              |||||||||||||||||
Db        502 GCACCGGTGCAGGGGGG 518


RESULT 3
CR086950/c
LOCUS       CR086950                  54 bp    DNA     linear   GSS 05-JUL-2004
DEFINITION  Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHPP370o19, genomic survey sequence.
ACCESSION   CR086950
VERSION     CR086950.1  GI:49820542
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPP370o19"
                     /clone_lib="MHPP"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 54;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||| |||||||||||||||
Db         33 TGCTCCGGTGCAGGGGGG 16


RESULT 4
AW325275/c
LOCUS       AW325275                  245 bp    mRNA    linear   EST 21-SEP-2000
DEFINITION  TENU4637 T.cruzi epimastigote normalized cDNA Library Trypanosoma
            cruzi cDNA clone 25h9 5', mRNA sequence.
ACCESSION   AW325275
VERSION     AW325275.1  GI:6761196
KEYWORDS    EST.
SOURCE      Trypanosoma cruzi
  ORGANISM  Trypanosoma cruzi
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma; Schizotrypanum.
REFERENCE   1  (bases 1 to 245)
  AUTHORS   Porcel,B.M., Tran,A.-N., Tammi,M., Nyarady,Z., Rydaker,M.,
            Urmenyi,T.P., Rondinelli,E., Pettersson,U., Andersson,B. and
            Aslund,L.
  TITLE     Gene survey of the pathogenic protozoan Trypanosoma cruzi
  JOURNAL   Genome Res. 10 (8), 1103-1107 (2000)
  MEDLINE   20414748
   PUBMED   10958628
COMMENT     Contact: Aslund L
            Department of Medical Genetics
            Uppsala University
            Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
            Tel: 46 18 471 45 85
            Fax: 46 18 52 68 49
            Email: lena.aslund@medgen.uu.se
            Seq primer: T7 primer
            High quality sequence stop: 245.
FEATURES             Location/Qualifiers
     source          1. .245
                     /organism="Trypanosoma cruzi"
                     /mol_type="mRNA"
                     /strain="Cl-Brenner"
                     /db_xref="taxon:5693"
                     /clone="25h9"
                     /cell_type="epimastigote"
                     /clone_lib="T.cruzi epimastigote normalized cDNA Library"
                     /note="cDNA library constructed with oligo dt primed
                     epimastigote mRNA and cloned in pt7t318D phagemid with
                     modified polylinker (Pharmacia)"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 2;  Length 245;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||| |||||||||||||
Db         65 TGCATCGGTGCAGGGGGG 48


RESULT 5
AQ444154/c
LOCUS       AQ444154                  277 bp    DNA     linear   GSS 09-JAN-2001
DEFINITION  GSSTc0207 Trypanosoma cruzi random genomic library Trypanosoma
            cruzi genomic clone G10L7, genomic survey sequence.
ACCESSION   AQ444154
VERSION     AQ444154.3  GI:10130745
KEYWORDS    GSS.
SOURCE      Trypanosoma cruzi
  ORGANISM  Trypanosoma cruzi
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
```

```
            Trypanosoma; Schizotrypanum.
REFERENCE   1  (bases 1 to 277)
  AUTHORS   Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
  TITLE     A random sequencing approach for the analysis of the trypanosoma
            cruzi genome: general structure, large gene and repetitive DNA
            families, and gene discovery
  JOURNAL   Genome Res. 10 (12), 1996-2005 (2000)
  MEDLINE   20568489
   PUBMED   11116094
COMMENT     On Sep 14, 2000 this sequence version replaced gi:9372108.
            Contact: Sanchez D.O.
            Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
            Aires, Argentina
            Tel: (54-11) 4580/7255/7
            Fax: (54-11) 4752-9639
            Email: dsanchez@iib.unsam.edu.ar
            Sequences were basecalled with phred and vector was masked with
            crossmatch (see http://genome.washington.edu). Sequences were then
            trimmed from both ends to remove low quality bases and masked
            vector.
            Seq primer: T7
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .277
                     /organism="Trypanosoma cruzi"
                     /mol_type="genomic DNA"
                     /strain="CL-Brener"
                     /db_xref="taxon:5693"
                     /clone="G10L7"
                     /cell_type="epimastigote"
                     /clone_lib="Trypanosoma cruzi random genomic library"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
                     randomly sheared using a nebulizer and the 1 to 2 Kb range
                     was gel purified and cloned into the dephosphoryated
                     HincII site of the vector"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 8;  Length 277;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||| ||||||||||||
Db        238 TGCATCGGTGCAGGGGGG 221


RESULT 6
CB076094/c
LOCUS       CB076094                339 bp    mRNA    linear   EST 24-JAN-2003
DEFINITION  hf37c06.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
            terminalis cDNA clone hf37c06, mRNA sequence.
ACCESSION   CB076094
VERSION     CB076094.1  GI:27889531
KEYWORDS    EST.
SOURCE      Hedyotis terminalis
  ORGANISM  Hedyotis terminalis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
            Spermacoceae; Hedyotis.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P. and Stevenson,D.
  TITLE     Expressed tag sequences from Hedyotis terminalis flower - Stage 2
            (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hf37  row: c  column: 06
            Seq primer: -21M13UnivRev
            High quality sequence stop: 339.
FEATURES             Location/Qualifiers
     source          1. .339
                     /organism="Hedyotis terminalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:219667"
                     /clone="hf37c06"
                     /dev_stage="pre-anthesis; Stage 2"
                     /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
                     /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
                     Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
                     CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
                     Synthesis Kit. The library was size-fractionated to enrich
                     for large inserts. Sample: collected on the island of
                     Hawaii, Hawaii; NYBG herbarium voucher TM2562"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 339;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||| ||||||||||||
Db         97 TGCACTGGTGCAGGGGGG 80


RESULT 7
CB087291/c
LOCUS       CB087291                440 bp    mRNA    linear   EST 27-JAN-2003
DEFINITION  hj98g11.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
            centranthoides cDNA clone hj98g11, mRNA sequence.
ACCESSION   CB087291
VERSION     CB087291.1  GI:27911483
KEYWORDS    EST.
SOURCE      Hedyotis centranthoides
  ORGANISM  Hedyotis centranthoides
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
            Spermacoceae; Hedyotis.
REFERENCE   1  (bases 1 to 440)
  AUTHORS   Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P. and Stevenson,D.
  TITLE     Expressed tag sequences from Hedyotis centranthoides flower - Stage
            2 (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hj98  row: g  column: 11
            Seq primer: -21M13UnivRev
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .440
                     /organism="Hedyotis centranthoides"
                     /mol_type="mRNA"
                     /db_xref="taxon:219666"
                     /clone="hj98g11"
                     /dev_stage="pre-anthesis; Stage 2"
                     /clone_lib="Hedyotis centranthoides flower - Stage 2
                     (NYBG)"
                     /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
                     Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
```

CSHL 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 440;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||||||||
Db        129 TGCACTGGTGCAGGGGGG 112
```

RESULT 8
CB087214/c
LOCUS CB087214 509 bp mRNA linear EST 27-JAN-2003
DEFINITION hj97e04.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis centranthoides cDNA clone hj97e04, mRNA sequence.
ACCESSION CB087214
VERSION CB087214.1 GI:27911406
KEYWORDS EST.
SOURCE Hedyotis centranthoides
ORGANISM Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Rubiaceae; Rubioideae; Spermacoceae; Hedyotis.
REFERENCE 1 (bases 1 to 509)
AUTHORS Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D.
TITLE Expressed tag sequences from Hedyotis centranthoides flower - Stage 2 (NYBG)
JOURNAL Unpublished (2003)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hj97 row: e column: 04
Seq primer: -21M13UnivRev
High quality sequence stop: 509.
FEATURES Location/Qualifiers
source 1. .509
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone="hj97e04"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2 (NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date: Completed 12/18/01. Submitted to CSHL 12/21/01 Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: collected on the island of Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 509;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||||||||
Db        144 TGCACTGGTGCAGGGGGG 127
```

RESULT 9
AI370313
LOCUS AI370313 562 bp mRNA linear EST 15-FEB-1999
DEFINITION qv76e01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:1987512 3' similar to TR:Q13045 Q13045 FLII ;, mRNA sequence.
ACCESSION AI370313
VERSION AI370313.1 GI:4149066
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 562)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1872 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.
FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1987512"
/tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN

Query Match 91.1%; Score 16.4; DB 1; Length 562;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TGCACCGGTGCAGGGGGG 18
              |||||||||||||| ||||
Db        509 TGCACCGGTGCAGAGGGG 526
```

RESULT 10
CB087525/c
LOCUS CB087525 598 bp mRNA linear EST 27-JAN-2003
DEFINITION hk03f05.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis centranthoides cDNA clone hk03f05, mRNA sequence.
ACCESSION CB087525
VERSION CB087525.1 GI:27911717
KEYWORDS EST.
SOURCE Hedyotis centranthoides
ORGANISM Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Rubiaceae; Rubioideae; Spermacoceae; Hedyotis.
REFERENCE 1 (bases 1 to 598)
AUTHORS Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D.
TITLE Expressed tag sequences from Hedyotis centranthoides flower - Stage

```
            2 (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: hk03  row: f  column: 05
            Seq primer: -21M13UnivRev
            High quality sequence stop: 598.
FEATURES             Location/Qualifiers
     source          1. .598
                     /organism="Hedyotis centranthoides"
                     /mol_type="mRNA"
                     /db_xref="taxon:219666"
                     /clone="hk03f05"
                     /dev_stage="pre-anthesis; Stage 2"
                     /clone_lib="Hedyotis centranthoides flower - Stage 2
                     (NYBG)"
                     /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
                     Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
                     CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
                     Synthesis Kit. The library was size-fractionated to enrich
                     for large inserts. Sample: collected on the island of
                     Hawaii, Hawaii; NYBG herbarium voucher TM2563"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 598;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||||||||
Db        146 TGCACTGGTGCAGGGGGG 129


RESULT 11
CG692380
LOCUS       CG692380                610 bp    DNA     linear   GSS 14-OCT-2003
DEFINITION  ZMMBBb0292G11.f ZMMBBb Zea mays genomic clone ZMMBBb0292G11 5',
            genomic survey sequence.
ACCESSION   CG692380
VERSION     CG692380.1  GI:37656062
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
            and Wing,R.
  TITLE     Sequencing of the maize genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: M13r
            Plate: 0292  row: G  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBBb0292G11"
                     /lab_host="DH10B"
                     /clone_lib="ZMMBBb"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Zea mays L. ssp. mays"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 610;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||| ||||||||
Db        525 TGCACCGGTTCAGGGGGG 542


RESULT 12
CN788545/c
LOCUS       CN788545                665 bp    mRNA    linear   EST 26-MAY-2004
DEFINITION  4122892 BARC 8BOV Bos taurus cDNA clone 8BOV_27I18 5', mRNA
            sequence.
ACCESSION   CN788545
VERSION     CN788545.1  GI:47684525
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 665)
  AUTHORS   Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
            Matukumalli,L.K.
  TITLE     Construction and Analysis of a cDNA Library Generated From
            Intestinal Muscle and Epithelial Tissues of Holstein Cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Richard G. Baumann
            Bovine Functional Genomics Lab
            ANRI
            BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
            Tel: 3015048604
            Fax: 3015048744
            Email: rbaumann@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt '' -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 18
            Plate: 27  row: I  column: 18
            Seq primer: CCTATTTAGGTGACACTATAGAAC
            High quality sequence stop: 665.
FEATURES             Location/Qualifiers
     source          1. .665
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="8BOV_27I18"
                     /sex="Female"
                     /tissue_type="Epithelial, Muscle"
                     /dev_stage="Lactating, Neonatal"
                     /lab_host="DH10B TonA"
                     /clone_lib="BARC 8BOV"
                     /note="Organ: Intestine; Vector: pCMVSport6.1; Site_1:
                     NotI; Site_2: EcoRI; Normalized cow cDNA intestinal
                     library in pCMVsport6.1, constructed from equimolar mRNA
                     pools derived from 5 sources, 4 lactating intestinal, 1
                     neonatal intestinal 4/5 Lactating, Proximal Duodenum,
                     Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
                     Duodenum, Jejunum, Distal Ileum"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 7;  Length 665;
```

```
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||||||||||||| |||
Db        117 TGCACCGGTGCAGGAGGG 100


RESULT 13
BM624520/c
LOCUS       BM624520                684 bp    mRNA    linear   EST 26-FEB-2002
DEFINITION  17000687491457 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
            19600449632784 5', mRNA sequence.
ACCESSION   BM624520
VERSION     BM624520.1  GI:18924031
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
            Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltRA@celera.com
            Plate: NU01004ABX  row: I  column: 06
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
                     chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449632784"
                     /dev_stage="Adult"
                     /lab_host="DH10b"
                     /clone_lib="A.Gam.ad.cDNA1"
                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen.
                     cDNA  inserts >500 bp cloned directionally into pSport 1.
                     Not 1 site is  3'. Clones available through the Malaria
                     Research and Reference  Reagent Resource Center
                     (www.malaria.mr4.org)."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 4;  Length 684;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||||||||||| |||||
Db        168 TGCACCGGTGCACGGGGG 151


RESULT 14
BM620160/c
LOCUS       BM620160                692 bp    mRNA    linear   EST 25-FEB-2002
DEFINITION  17000687442189 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
            19600449668094 5', mRNA sequence.
ACCESSION   BM620160
VERSION     BM620160.1  GI:18918578
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
            Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltRA@celera.com
            Plate: NU01004ABH  row: H  column: 12
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
                     chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449668094"
                     /dev_stage="Adult"
                     /lab_host="DH10b"
                     /clone_lib="A.Gam.ad.cDNA1"
                     /note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen.
                     cDNA  inserts >500 bp cloned directionally into pSport 1.
                     Not 1 site is  3'. Clones available through the Malaria
                     Research and Reference  Reagent Resource Center
                     (www.malaria.mr4.org)."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 4;  Length 692;
  Best Local Similarity   94.4%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              |||||||||||| |||||
Db        183 TGCACCGGTGCACGGGGG 166


RESULT 15
BM621890/c
LOCUS       BM621890                708 bp    mRNA    linear   EST 25-FEB-2002
DEFINITION  17000687447901 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
            19600449620865 5', mRNA sequence.
ACCESSION   BM621890
VERSION     BM621890.1  GI:18920308
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
            Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
  TITLE     Celera Anopheles gambiae EST project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celera Genomics
            45 w. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltRA@celera.com
            Plate: NU01004NBU  row: H  column: 15
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
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/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449620865"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site_1: Sal1; Site_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 91.1%; Score 16.4; DB 4; Length 708;
Best Local Similarity 94.4%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||| |||||
Db        153 TGCACCGGTGCACGGGGG 136
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Search completed: April 29, 2005, 11:55:17
Job time : 1689.62 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 52.6622 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-13
Perfect score: 18
Sequence: 1 tgcaccggtgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15.4	85.6	7353	4	US-09-949-016-14895	Sequence 14895, A
	2	14.8	82.2	601	4	US-09-949-016-19926	Sequence 19926, A
c	3	14.8	82.2	601	4	US-09-949-016-26092	Sequence 26092, A
c	4	14.8	82.2	601	4	US-09-949-016-26093	Sequence 26093, A
c	5	14.8	82.2	601	4	US-09-949-016-26094	Sequence 26094, A
	6	14.8	82.2	601	4	US-09-949-016-46188	Sequence 46188, A
c	7	14.8	82.2	601	4	US-09-949-016-198863	Sequence 198863,
c	8	14.8	82.2	601	4	US-09-949-016-198864	Sequence 198864,
c	9	14.8	82.2	601	4	US-09-949-016-198865	Sequence 198865,
c	10	14.8	82.2	601	4	US-09-949-016-201687	Sequence 201687,
	11	14.8	82.2	1432	4	US-09-902-540-264	Sequence 264, App
	12	14.8	82.2	1432	4	US-09-902-540-6080	Sequence 6080, Ap
c	13	14.8	82.2	1443	3	US-08-959-381A-3	Sequence 3, Appli
c	14	14.8	82.2	1446	4	US-09-170-496D-81	Sequence 81, Appl
c	15	14.8	82.2	1446	4	US-09-170-496D-207	Sequence 207, App
c	16	14.8	82.2	1626	3	US-08-959-381A-4	Sequence 4, Appli
	17	14.8	82.2	3358	3	US-09-248-571-2	Sequence 2, Appli
	18	14.8	82.2	3358	3	US-09-553-736-2	Sequence 2, Appli
	19	14.8	82.2	22927	4	US-09-949-016-11849	Sequence 11849, A
	20	14.8	82.2	22928	4	US-09-949-016-13071	Sequence 13071, A
	21	14.8	82.2	24707	4	US-09-740-027-3	Sequence 3, Appli
	22	14.8	82.2	24720	4	US-09-949-016-12341	Sequence 12341, A
	23	14.8	82.2	24721	4	US-09-949-016-15610	Sequence 15610, A
	24	14.8	82.2	36938	4	US-09-949-016-13484	Sequence 13484, A
c	25	14.8	82.2	38653	4	US-09-922-445-1	Sequence 1, Appli
c	26	14.8	82.2	139150	4	US-09-949-016-17398	Sequence 17398, A
c	27	14.8	82.2	139577	4	US-09-949-016-12879	Sequence 12879, A
	28	14.8	82.2	767677	4	US-09-949-016-12147	Sequence 12147, A
	29	14.8	82.2	767677	4	US-09-949-016-17361	Sequence 17361, A
	30	14.4	80.0	265	4	US-09-313-294A-385	Sequence 385, App
c	31	14.4	80.0	601	4	US-09-949-016-117679	Sequence 117679,
	32	14.4	80.0	771	4	US-09-902-540-8490	Sequence 8490, Ap
c	33	14.4	80.0	1446	4	US-09-902-540-5188	Sequence 5188, Ap
	34	14.4	80.0	2194	4	US-09-023-655-668	Sequence 668, App
	35	14.4	80.0	12955	4	US-09-902-540-1068	Sequence 1068, Ap
	36	14.4	80.0	15133	4	US-09-949-016-15001	Sequence 15001, A
c	37	14.4	80.0	24638	4	US-09-949-016-12087	Sequence 12087, A
c	38	14.4	80.0	24639	4	US-09-949-016-15749	Sequence 15749, A
	39	14.4	80.0	34199	4	US-09-902-540-1255	Sequence 1255, Ap
c	40	14.4	80.0	90776	4	US-09-949-016-17230	Sequence 17230, A
c	41	14.4	80.0	194889	4	US-09-949-016-15654	Sequence 15654, A
	42	14	77.8	732	4	US-09-252-991A-736	Sequence 736, App
c	43	14	77.8	1350	4	US-09-252-991A-677	Sequence 677, App
c	44	14	77.8	7168	3	US-08-840-316-4	Sequence 4, Appli
c	45	14	77.8	7168	3	US-08-809-523-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-14895/c
; Sequence 14895, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14895
; LENGTH: 7353
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(7353)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14895

Query Match 85.6%; Score 15.4; DB 4; Length 7353;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 GCACCGGTGCAGGGGGG 18
              ||| |||||||||||||
Db        645 GCAGCGGTGCAGGGGGG 629
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RESULT 2
US-09-949-016-19926
; Sequence 19926, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19926
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-19926

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| || |||||||||
Db        312 TGCACTGGGGCAGGGGGG 329


RESULT 3
US-09-949-016-26092/c
; Sequence 26092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26092
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-26092

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||| ||||
Db        551 TGCACGGGTGCAGAGGGG 534


RESULT 4
US-09-949-016-26093/c
; Sequence 26093, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26093
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-26093

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||| ||||
Db        445 TGCACGGGTGCAGAGGGG 428


RESULT 5
US-09-949-016-26094/c
; Sequence 26094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26094
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-26094

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||| ||||
Db         69 TGCACGGGTGCAGAGGGG 52


RESULT 6
US-09-949-016-46188
; Sequence 46188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46188
;   LENGTH: 601
;   TYPE: DNA
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;   ORGANISM: Human
US-09-949-016-46188

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| || ||||||||||
Db        312 TGCACTGGGGCAGGGGGG 329


RESULT 7
US-09-949-016-198863/c
; Sequence 198863, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198863
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-198863

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||| ||||
Db        551 TGCACGGGTGCAGAGGGG 534


RESULT 8
US-09-949-016-198864/c
; Sequence 198864, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198864
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-198864

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||| ||||
Db        445 TGCACGGGTGCAGAGGGG 428


RESULT 9
US-09-949-016-198865/c
; Sequence 198865, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198865
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-198865

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||| ||||||| ||||
Db         69 TGCACGGGTGCAGAGGGG 52


RESULT 10
US-09-949-016-201687/c
; Sequence 201687, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201687
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-201687

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              | |||| ||||||||||
Db        537 TTCACCCGTGCAGGGGGG 520
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RESULT 11
US-09-902-540-264
; Sequence 264, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 264
;   LENGTH: 1432
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-264

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 1432;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||| |||||||||| ||||
Db        930 TGCCCCGGTGCAGTGGGG 947


RESULT 12
US-09-902-540-6080
; Sequence 6080, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6080
;   LENGTH: 1432
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-6080

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 1432;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||| |||||||||| ||||
Db        930 TGCCCCGGTGCAGTGGGG 947


RESULT 13
US-08-959-381A-3/c
; Sequence 3, Application US/08959381A
; Patent No. 6048711
;  GENERAL INFORMATION:
;    APPLICANT:  HINUMA, SHUJI
;    APPLICANT:  FUKUSUMI, SHOJI
;    APPLICANT:  KAWAMATA, YUJI
;    TITLE OF INVENTION:  NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
;    TITLE OF INVENTION:  POLYNUCLEOTIDES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ratner & Prestia
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/959,381A
;      FILING DATE:  28-OCT-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  286823/1996
;      FILING DATE:  29-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Prestia, Paul F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  TAK-50003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0700
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1443 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-959-381A-3

  Query Match             82.2%;  Score 14.8;  DB 3;  Length 1443;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||| | ||||||||||||||
Db         94 TGCCCAGGTGCAGGGGGG 77


RESULT 14
US-09-170-496D-81/c
; Sequence 81, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
;   LENGTH: 1446
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-170-496D-81

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 1446;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
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              ||| | ||||||||||||
Db         94 TGCCCAGGTGCAGGGGGG 77


RESULT 15
US-09-170-496D-207/c
; Sequence 207, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 207
;   LENGTH: 1446
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-170-496D-207

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 1446;
  Best Local Similarity   88.9%;  Pred. No. 6.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||| | ||||||||||||
Db         94 TGCCCAGGTGCAGGGGGG 77


Search completed: April 29, 2005, 12:02:40
Job time : 54.7872 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 241.419 Seconds
(without alignments)
453.893 Million cell updates/sec

Title: US-10-068-160A-13
Perfect score: 18
Sequence: 1 tgcaccggtgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	14	US-10-068-160-13	Sequence 13, Appl
2	18	100.0	20	11	US-09-874-991C-496	Sequence 496, App
3	18	100.0	20	11	US-09-874-991C-504	Sequence 504, App
4	18	100.0	20	11	US-09-874-991C-507	Sequence 507, App
5	18	100.0	20	11	US-09-874-991C-514	Sequence 514, App
6	18	100.0	20	11	US-09-874-991C-540	Sequence 540, App
7	18	100.0	20	14	US-10-068-160-2	Sequence 2, Appli
8	18	100.0	20	15	US-10-194-035-42	Sequence 42, Appl
9	18	100.0	20	18	US-10-666-022-2	Sequence 2, Appli
10	18	100.0	20	18	US-10-666-022-178	Sequence 178, App
11	18	100.0	20	18	US-10-486-755-2	Sequence 2, Appli
12	18	100.0	20	18	US-10-486-755-6	Sequence 6, Appli
13	18	100.0	20	18	US-10-486-755-19	Sequence 19, Appl
14	18	100.0	20	19	US-10-499-597-13	Sequence 13, Appl
15	18	100.0	28	11	US-09-874-991C-517	Sequence 517, App
16	18	100.0	28	11	US-09-874-991C-525	Sequence 525, App
17	18	100.0	28	11	US-09-874-991C-529	Sequence 529, App
18	18	100.0	28	11	US-09-874-991C-537	Sequence 537, App
19	18	100.0	40	11	US-09-874-991C-548	Sequence 548, App
c 20	17	94.4	432	18	US-10-425-115-150828	Sequence 150828,
c 21	17	94.4	940	18	US-10-425-115-169731	Sequence 169731,
22	16.4	91.1	20	11	US-09-874-991C-495	Sequence 495, App
23	16.4	91.1	20	11	US-09-874-991C-499	Sequence 499, App
24	16.4	91.1	20	11	US-09-874-991C-506	Sequence 506, App
25	16.4	91.1	20	11	US-09-874-991C-510	Sequence 510, App
26	16.4	91.1	20	11	US-09-874-991C-543	Sequence 543, App
27	16.4	91.1	20	14	US-10-068-160-37	Sequence 37, Appl
28	16.4	91.1	20	14	US-10-068-160-58	Sequence 58, Appl
29	16.4	91.1	20	15	US-10-194-035-101	Sequence 101, App
30	16.4	91.1	20	18	US-10-486-755-17	Sequence 17, Appl
31	16.4	91.1	20	18	US-10-486-755-26	Sequence 26, Appl
32	16.4	91.1	20	18	US-10-486-755-27	Sequence 27, Appl
33	16.4	91.1	20	19	US-10-499-597-23	Sequence 23, Appl
34	16.4	91.1	20	19	US-10-499-597-40	Sequence 40, Appl
35	16.4	91.1	28	11	US-09-874-991C-516	Sequence 516, App
36	16.4	91.1	28	11	US-09-874-991C-520	Sequence 520, App
37	16.4	91.1	28	11	US-09-874-991C-528	Sequence 528, App
38	16.4	91.1	28	11	US-09-874-991C-532	Sequence 532, App
39	15.4	85.6	19	15	US-10-194-035-22	Sequence 22, Appl
40	15.4	85.6	198	18	US-10-437-963-71085	Sequence 71085, A
c 41	15.4	85.6	349	10	US-09-764-891-1439	Sequence 1439, Ap
42	15.4	85.6	438	18	US-10-437-963-15540	Sequence 15540, A
c 43	15.4	85.6	466	13	US-10-027-632-46784	Sequence 46784, A
c 44	15.4	85.6	466	17	US-10-027-632-46784	Sequence 46784, A
45	15.4	85.6	473	18	US-10-425-115-168719	Sequence 168719,

ALIGNMENTS

RESULT 1
US-10-068-160-13
; Sequence 13, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-13

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCACCGGTGCAGGGGGG 18
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Db          1 TGCACCGGTGCAGGGGGG 18
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RESULT 2
US-09-874-991C-496
; Sequence 496, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-496

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 3
US-09-874-991C-504
; Sequence 504, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 504
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-504

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 4
US-09-874-991C-507
; Sequence 507, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 507
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-507

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 5
US-09-874-991C-514
; Sequence 514, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 514
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-514

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 6
US-09-874-991C-540
; Sequence 540, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
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;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 540
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-540

  Query Match             100.0%;  Score 18;  DB 11;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 7
US-10-068-160-2
; Sequence 2, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-2

  Query Match             100.0%;  Score 18;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 8
US-10-194-035-42
; Sequence 42, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42

  Query Match             100.0%;  Score 18;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 9
US-10-666-022-2
; Sequence 2, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISE
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(20)
;   OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-2

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 10
US-10-666-022-178
; Sequence 178, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISE
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
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;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 178
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: synthetic
US-10-666-022-178

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 11
US-10-486-755-2
; Sequence 2, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-486-755-2

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
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Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 12
US-10-486-755-6
; Sequence 6, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: CpG oligodeoxynucleotide
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)..(2)
;    OTHER INFORMATION: n is any base, or is no base at all
US-10-486-755-6

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
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Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 13
US-10-486-755-19
; Sequence 19, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-486-755-19

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  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCACCGGTGCAGGGGGG 18
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Db          3 TGCACCGGTGCAGGGGGG 20


RESULT 14
US-10-499-597-13
; Sequence 13, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
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; APPLICANT: Rouse, Barry T.
; APPLICANT: Zheng, Mei
; TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
; FILE REFERENCE: 4239-64125-02
; CURRENT APPLICATION NUMBER: US/10/499,597
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: PCT/US02/40955
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/343,457
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG D oligonucleotide
US-10-499-597-13

Query Match 100.0%; Score 18; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGGG 18
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Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 15
US-09-874-991C-517
; Sequence 517, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-517

Query Match 100.0%; Score 18; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 TGCACCGGTGCAGGGGGG 20

Search completed: April 29, 2005, 12:35:41
Job time : 242.419 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 712.216 Seconds
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1224.620 Million cell updates/sec

Title: US-10-068-160A-14
Perfect score: 18
Sequence: 1 tgcgtcgacgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	20	6	AX194439	AX194439 Sequence
2	18	100.0	20	6	AX194441	AX194441 Sequence
3	18	100.0	20	6	AX465389	AX465389 Sequence
4	18	100.0	20	6	AX465391	AX465391 Sequence
5	16.4	91.1	20	6	AX194440	AX194440 Sequence
6	16.4	91.1	20	6	AX194481	AX194481 Sequence
7	16.4	91.1	20	6	AX194482	AX194482 Sequence
8	16.4	91.1	20	6	AX194500	AX194500 Sequence
9	16.4	91.1	20	6	AX352202	AX352202 Sequence
10	16.4	91.1	20	6	AX352213	AX352213 Sequence
11	16.4	91.1	20	6	AX352246	AX352246 Sequence
12	16.4	91.1	20	6	AX465390	AX465390 Sequence
13	16.4	91.1	20	6	AX465431	AX465431 Sequence
14	16.4	91.1	20	6	AX465432	AX465432 Sequence
15	16.4	91.1	28	6	AX352223	AX352223 Sequence
16	16.4	91.1	28	6	AX352235	AX352235 Sequence
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c 19	16.4	91.1	110000	1	CP000010_15	Continuation (16 o
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23	16	88.9	320	11	BV137299	BV137299 PZA00073
24	16	88.9	342	11	BV137315	BV137315 PZA00073
25	16	88.9	343	11	BV137311	BV137311 PZA00073
26	16	88.9	344	11	BV137317	BV137317 PZA00073
27	16	88.9	348	11	BV137318	BV137318 PZA00073
28	16	88.9	349	11	BV137308	BV137308 PZA00073
29	16	88.9	352	11	BV137304	BV137304 PZA00073
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40	15.4	85.6	19	6	AX194483	AX194483 Sequence
41	15.4	85.6	19	6	AX194488	AX194488 Sequence
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ALIGNMENTS

RESULT 1
AX194439
LOCUS AX194439 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 39 from Patent WO0151500.
ACCESSION AX194439
VERSION AX194439.1 GI:15385095
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 39 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
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Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 2
AX194441
LOCUS AX194441 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 41 from Patent WO0151500.
ACCESSION AX194441
VERSION AX194441.1 GI:15385097
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 41 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 3
AX465389
LOCUS       AX465389                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 57 from Patent WO0211761.
ACCESSION   AX465389
VERSION     AX465389.1  GI:21899752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 57 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 4
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LOCUS       AX465391                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 59 from Patent WO0211761.
ACCESSION   AX465391
VERSION     AX465391.1  GI:21899754
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 59 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 5
AX194440
LOCUS       AX194440                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 40 from Patent WO0151500.
ACCESSION   AX194440
VERSION     AX194440.1  GI:15385096
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 40 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
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Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 6
AX194481
LOCUS       AX194481                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 81 from Patent WO0151500.
ACCESSION   AX194481
VERSION     AX194481.1  GI:15385137
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 81 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
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Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 7
AX194482
LOCUS       AX194482                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 82 from Patent WO0151500.
ACCESSION   AX194482
VERSION     AX194482.1  GI:15385138
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 82 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||| |||||||||
Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 8
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LOCUS       AX194500                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 100 from Patent WO0151500.
ACCESSION   AX194500
VERSION     AX194500.1  GI:15385156
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 100 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCATCGACGCAGGGGGG 20


RESULT 9
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LOCUS       AX352202                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 498 from Patent WO0193902.
ACCESSION   AX352202
VERSION     AX352202.1  GI:18617485
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 498 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCATCGACGCAGGGGGG 20


RESULT 10
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LOCUS       AX352213                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 509 from Patent WO0193902.
ACCESSION   AX352213
VERSION     AX352213.1  GI:18617496
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 509 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCATCGACGCAGGGGGG 20


RESULT 11
AX352246
LOCUS       AX352246                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 542 from Patent WO0193902.
ACCESSION   AX352246
VERSION     AX352246.1  GI:18617529
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
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  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 542 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||| ||||||||||||||
Db          3 TGCATCGACGCAGGGGGG 20


RESULT 12
AX465390
LOCUS       AX465390                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 58 from Patent WO0211761.
ACCESSION   AX465390
VERSION     AX465390.1  GI:21899753
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 58 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||| |||||||||
Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 13
AX465431
LOCUS       AX465431                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 99 from Patent WO0211761.
ACCESSION   AX465431
VERSION     AX465431.1  GI:21899794
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 99 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||| |||||||||
Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 14
AX465432
LOCUS       AX465432                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 100 from Patent WO0211761.
ACCESSION   AX465432
VERSION     AX465432.1  GI:21899795
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 100 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 3.4e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||| |||||||||
Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 15
AX352223
LOCUS       AX352223                  28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 519 from Patent WO0193902.
ACCESSION   AX352223
VERSION     AX352223.1  GI:18617506
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 519 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 TGCGTCGACGCAGGGGGG 18
              ||| ||||||||||||||
Db          3 TGCATCGACGCAGGGGGG 20
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Search completed: April 29, 2005, 08:03:46
Job time : 713.341 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 183.527 Seconds
(without alignments)
580.598 Million cell updates/sec

Title: US-10-068-160A-14
Perfect score: 18
Sequence: 1 tgcgtcgacgcaggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: geneseqn2002bs:*
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9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	20	4	AAC80619	Aac80619 Immunogen
2	18	100.0	20	4	AAC80621	Aac80621 Immunogen
3	18	100.0	20	4	AAS09591	Aas09591 Immunorea
4	18	100.0	20	4	AAS09589	Aas09589 Immunorea
5	18	100.0	20	6	ABK46469	Abk46469 Immunosti
6	18	100.0	20	6	ABK46467	Abk46467 Immunosti
7	18	100.0	20	8	ACC48301	Acc48301 CpG oligo
8	18	100.0	20	8	ACC48315	Acc48315 CpG oligo
9	18	100.0	20	9	ACC83120	Acc83120 D class C
10	18	100.0	20	10	ADD01055	Add01055 CpG D oli
11	18	100.0	20	12	ADN96869	Adn96869 Immunosti
12	16.4	91.1	20	4	AAC80662	Aac80662 Immunogen
13	16.4	91.1	20	4	AAC80661	Aac80661 Immunogen
14	16.4	91.1	20	4	AAC80620	Aac80620 Immunogen
15	16.4	91.1	20	4	AAS09650	Aas09650 Immunorea
16	16.4	91.1	20	4	AAS09631	Aas09631 Immunorea
17	16.4	91.1	20	4	AAS09590	Aas09590 Immunorea
18	16.4	91.1	20	4	AAS09632	Aas09632 Immunorea
19	16.4	91.1	20	6	ABL35616	Abl35616 Immunosti
20	16.4	91.1	20	6	ABL35572	Abl35572 Immunosti
21	16.4	91.1	20	6	ABL35583	Abl35583 Immunosti
22	16.4	91.1	20	6	ABK46510	Abk46510 Immunosti
23	16.4	91.1	20	6	ABK46468	Abk46468 Immunosti
24	16.4	91.1	20	6	ABK46509	Abk46509 Immunosti
25	16.4	91.1	20	8	ACC48298	Acc48298 CpG oligo
26	16.4	91.1	20	8	ACC48312	Acc48312 CpG oligo
27	16.4	91.1	20	8	ACC48314	Acc48314 CpG oligo
28	16.4	91.1	20	8	ACC48304	Acc48304 CpG oligo
29	16.4	91.1	20	8	ACC48306	Acc48306 CpG oligo
30	16.4	91.1	20	8	ACC48319	Acc48319 CpG oligo
31	16.4	91.1	20	9	ACC83119	Acc83119 D class C
32	16.4	91.1	20	9	ACC83117	Acc83117 D class C
33	16.4	91.1	20	9	ACC83124	Acc83124 D class C
34	16.4	91.1	20	10	ADD01050	Add01050 CpG D oli
35	16.4	91.1	20	10	ADD01057	Add01057 CpG D oli
36	16.4	91.1	20	12	ADN96882	Adn96882 Immunosti
37	16.4	91.1	20	12	ADN96870	Adn96870 Immunosti
38	16.4	91.1	20	12	ADN96873	Adn96873 Immunosti
39	16.4	91.1	28	6	ABL35605	Abl35605 Immunosti
40	16.4	91.1	28	6	ABL35593	Abl35593 Immunosti
c 41	16.4	91.1	34115	8	AAL56708	Aal56708 Rhesus mo
42	15.4	85.6	19	4	AAC80663	Aac80663 Immunogen
43	15.4	85.6	19	4	AAC80668	Aac80668 Immunogen
44	15.4	85.6	19	4	AAS09633	Aas09633 Immunorea
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ALIGNMENTS

RESULT 1
AAC80619
ID AAC80619 standard; DNA; 20 BP.
XX
AC AAC80619;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:39.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX

PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 2
AAC80621
ID AAC80621 standard; DNA; 20 BP.
XX
AC AAC80621;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:41.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 3

AAS09591
ID AAS09591 standard; DNA; 20 BP.
XX
AC AAS09591;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #41.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 34; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 4
AAS09589
ID AAS09589 standard; DNA; 20 BP.
XX
AC AAS09589;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #39.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 33; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

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  Query Match             100.0%;  Score 18;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 5
ABK46469
ID   ABK46469 standard; DNA; 20 BP.
XX
AC   ABK46469;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Immunostimulatory unmethylated CpG oligodideoxynucleotide #59.
XX
KW   unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW   Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW   viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW   bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS   Synthetic.
XX
PN   WO200211761-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US041633.
XX
PR   10-AUG-2000; 2000US-0224011P.
PR   01-SEP-2000; 2000US-0229307P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Mond JJ,  Prince G,  Klinman DM;
XX
DR   WPI; 2002-227118/28.
XX
PT   Vaccine for immunizing patient against respiratory syncytial virus, has
PT   epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT   linked by phosphate bond-oligodideoxynucleotides.
XX
PS   Claim 4; Page 8; 30pp; English.
XX
CC   The invention describes a vaccine comprising one or more epitopes of a
CC   Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC   guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC   vaccine is useful for vaccinating a patient especially against viruses of
CC   the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC   primary cause of viral bronchiolitis and pneumonia in infants and
CC   children, and infectious pulmonary disease in infants. RSV has been
CC   particularly implicated in death of infants that are premature, have
CC   bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC   represents an oligodideoxynucleotide that can be used in the creation of
CC   the vaccine
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 6
ABK46467
ID   ABK46467 standard; DNA; 20 BP.
XX
AC   ABK46467;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Immunostimulatory unmethylated CpG oligodideoxynucleotide #57.
XX
KW   unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW   Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW   viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW   bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS   Synthetic.
XX
PN   WO200211761-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US041633.
XX
PR   10-AUG-2000; 2000US-0224011P.
PR   01-SEP-2000; 2000US-0229307P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Mond JJ,  Prince G,  Klinman DM;
XX
DR   WPI; 2002-227118/28.
XX
PT   Vaccine for immunizing patient against respiratory syncytial virus, has
PT   epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT   linked by phosphate bond-oligodideoxynucleotides.
XX
PS   Claim 4; Page 8; 30pp; English.
XX
CC   The invention describes a vaccine comprising one or more epitopes of a
CC   Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC   guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC   vaccine is useful for vaccinating a patient especially against viruses of
CC   the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC   primary cause of viral bronchiolitis and pneumonia in infants and
CC   children, and infectious pulmonary disease in infants. RSV has been
CC   particularly implicated in death of infants that are premature, have
CC   bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC   represents an oligodideoxynucleotide that can be used in the creation of
CC   the vaccine
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 7
ACC48301
ID   ACC48301 standard; DNA; 20 BP.
XX
AC   ACC48301;
XX
DT   11-AUG-2003  (first entry)
XX
DE   CpG oligodeoxynucleotide used for dendritic cell maturation.
XX
KW   CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW   cytostatic; immunostimulant; gene therapy; ss.
XX
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   misc_difference 1
FT                   /*tag=  a
FT                   /note= "N is any base (especially G) or no base"
FT   misc_difference 2
FT                   /*tag=  b
FT                   /note= "N is any base (especially G) or no base"
XX
PN   WO2003020884-A2.
XX
PD   13-MAR-2003.
XX
PF   13-AUG-2002; 2002WO-US025732.
XX
PR   14-AUG-2001; 2001US-0312190P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel M,  Verthelyi D;
XX
DR   WPI; 2003-300874/29.
XX
PT   Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT   for activating the immune system to treat diseases such as cancer,
PT   comprises contacting a dendritic cell precursor with a D type
PT   oligodeoxynucleotide.
XX
PS   Disclosure; Page 26; 69pp; English.
XX
CC   The present sequence is that of a D type CpG oligodeoxynucleotide that is
CC   an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
CC   invention. Mature dendritic cells are obtained by contacting a dendritic
CC   cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
CC   The method is useful for generating mature dendritic cells and enhancing
CC   T cell responses, thus enhancing antigen presentation. Mature dendritic
CC   cells are useful for tumour immunotherapy, for augmenting an immune
CC   response to an infectious agent or to a vaccine, and as vaccines to
CC   prevent future infection or to activate the immune system to treat
CC   diseases such as cancer. Mature dendritic cells may also be used to
CC   produce activated T lymphocytes
XX
SQ   Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;

  Query Match             100.0%;  Score 18;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 8
ACC48315
ID   ACC48315 standard; DNA; 20 BP.
XX
AC   ACC48315;
XX
DT   11-AUG-2003  (first entry)
XX
DE   CpG oligodeoxynucleotide DV32.
XX
KW   CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW   cytostatic; immunostimulant; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   WO2003020884-A2.
XX
PD   13-MAR-2003.
XX
PF   13-AUG-2002; 2002WO-US025732.
XX
PR   14-AUG-2001; 2001US-0312190P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel M,  Verthelyi D;
XX
DR   WPI; 2003-300874/29.
XX
PT   Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT   for activating the immune system to treat diseases such as cancer,
PT   comprises contacting a dendritic cell precursor with a D type
PT   oligodeoxynucleotide.
XX
PS   Disclosure; Fig 8; 69pp; English.
XX
CC   The present sequence is that of CpG oligodeoxynucleotide DV32 of the
CC   invention. A claimed method for generating dendritic cells involves
CC   contacting a dendritic cell precursor, especially a monocyte, with a D
CC   type oligodeoxynucleotide (see ACC48294) containing a central
CC   unmethylated CpG motif. The method is useful for generating mature
CC   dendritic cells and enhancing T cell responses, thus enhancing antigen
CC   presentation. Mature dendritic cells are useful for tumour immunotherapy,
CC   for augmenting an immune response to an infectious agent or to a vaccine,
CC   and as vaccines to prevent future infection or to activate the immune
CC   system to treat diseases such as cancer. Mature dendritic cells may also
CC   be used to produce activated T lymphocytes
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 9
ACC83120
ID   ACC83120 standard; DNA; 20 BP.
XX
AC   ACC83120;
XX
DT   27-AUG-2003  (first entry)
XX
DE   D class CpG ODN sequence useful for encapsulating in SSCL, DV32.
XX
KW   Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW   tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW   thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW   schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW   asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW   CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW   multiple sclerosis; infection; tumour; ss.
XX
OS   Unidentified.
XX
PN   WO2003040308-A2.
XX
PD   15-MAY-2003.
XX
PF   29-JUL-2002; 2002WO-US024235.
XX
PR   27-JUL-2001; 2001US-0308283P.
PR   25-JUL-2002; 2002US-00206407.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Klinman DM,  Gursel I,  Ishii KJ,  Kawakami K,  Joshi BH,  Puri RK;
XX
DR   WPI; 2003-482260/45.
XX
```

PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10C; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 10
ADD01055
ID ADD01055 standard; DNA; 20 BP.
XX
AC ADD01055;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG D oligonucleotide SEQ ID NO:19.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerary; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
PN WO2003054161-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Zheng M, Rouse BT;
XX
DR WPI; 2003-559138/52.
XX
PT Inducing the production of vascular endothelial growth factor by a cell,
PT useful for inducing angiogenesis, comprises contacting the cell with a
PT CpG oligodeoxynucleotide.
XX
PS Example 7; SEQ ID NO 19; 37pp; English.
XX
CC The present invention describes a method for inducing the production of
CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC the cell with a CpG oligonucleotide and therefore inducing the production
CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC tissue, comprising introducing a CpG oligonucleotide into an area of the
CC tissue where the formation of new blood vessels is desired, and so
CC inducing neovascularisation in the area of the tissue; (2) promoting
CC angiogenesis in an area of the subject where angiogenesis is desired,
CC comprising introducing a CpG oligonucleotide to the area, and so
CC promoting angiogenesis in the subject; and (3) screening for an agent
CC that inhibits neovascularisation, comprising administering a CpG
CC oligonucleotide to a non-human mammal and administering the agent to the
CC mammal, where inhibition of angiogenesis in the animal indicates that the
CC agent is effective in inhibiting neovascularisation. The CpG
CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC activities, and can be used in gene therapy. The method and the CpG
CC oligonucleotides can be used in inducing angiogenesis or
CC neovascularisation, such as in subjects with a skin graft, subjects who
CC exhibit male pattern baldness, or subjects who have a wound or who have
CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a CpG oligonucleotide which is used in the exemplification of
CC the present invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 11
ADN96869
ID ADN96869 standard; DNA; 20 BP.
XX
AC ADN96869;
XX
DT 26-AUG-2004 (first entry)
XX
DE Immunostimulatory D CpG oligonucleotide seqid 3.
XX
KW virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;
KW tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;
KW dermatological; bacterial growth inhibitor; immunostimulator;
KW immune response; immunostimulatory; opportunistic infection;
KW lentivirus infection; human immunodeficiency virus infection; AIDS;
KW Leishmania infection; bacterial infection; fungal infection;
KW viral infection; protozoan infection; prion disease; nucleoplasm;
KW salmonellosis; syphilis; neurosyphilis; tuberculosis;
KW bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;
KW cryptococcal meningitis; hepatitis B; histoplasmosis; cryptosporidiosis;
KW isosporiasis; microsporidiosis; pneumocystis carinii pneumonia;
KW toxoplasmosis; cytomegalovirus; hepatitis; herpes simplex; herpes zoster;
KW human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;
KW progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;
KW systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;
KW HSV; genital herpes; HZV; shingles; genital wart; cervical cancer;
KW immunostimulatory CpG oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004105872-A1.
XX
PD 03-JUN-2004.
XX
PF 17-SEP-2003; 2003US-00666022.
XX

PR 18-SEP-2002; 2002US-0411944P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Verthelyi D;
XX
DR WPI; 2004-419442/39.
XX
PT Increasing an immune response to an opportunistic infection e.g.
PT bacterial infections in an immunocompromised subject involves
PT administering immunostimulatory D oligodeoxynucleotide or an
PT immunostimulatory K oligodeoxynucleotide.
XX
PS Claim 21; SEQ ID NO 3; 64pp; English.
XX
CC The invention describes a method of increasing an immune response to an
CC opportunistic infection in an immunocompromised subject involves
CC administering an immunostimulatory D oligodeoxynucleotide or an
CC immunostimulatory K oligodeoxynucleotide, where an antigenic epitope of a
CC polypeptide is not administered to the subject. The method is useful for
CC increasing an immune response to an opportunistic infection e.g.
CC infection with a lentivirus such as human immunodeficiency virus
CC (including HIV-1, HIV-2) e.g. AIDS; infection with Leishmania; bacterial
CC infections; fungal infections; viral infections; protozoan infections;
CC prion disease; and nucleoplasm in an immunocompromised subject or a
CC subject infected with a lentivirus. The bacterial infections include
CC salmonellosis, syphilis and neurosyphilis, tuberculosis and bacillary
CC angiomatosis, the fungal infections include aspergillosis, candidiasis,
CC coccidioidomycosis, cryptococcal meningitis, hepatitis B, and
CC histoplasmosis, the protozoal infections include cryptosporidiosis,
CC isosporiasis, microsporidiosis, pneumocystis carinii pneumonia and
CC toxoplasmosis, viral infections include cytomegalovirus, hepatitis,
CC herpes simplex, herpes zoster, human papilloma virus, molluscum
CC contagiosum, oral hairy leukoplakia and progressive multifocal
CC leukoencephalopathy and neoplasms include Kaposi's sarcoma, systemic non-
CC Hodgkin's lymphoma and primary central nervous system lymphoma. The
CC herpes simplex includes HSV, genital herpes. The herpes zoster includes
CC HZV and shingles. The human papilloma virus includes HPV, genital warts
CC and cervical cancer. The method stimulates immune responses to any
CC opportunistic infection in immunocompromised subjects. This sequence
CC represents an immunostimulatory CpG oligonucleotide sequence that
CC stimulate the release of cytokines from cells of the immune system and
CC can be used to increase immune response in the method of the invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGTCGACGCAGGGGGG 20

RESULT 12
AAC80662
ID AAC80662 standard; DNA; 20 BP.
XX
AC AAC80662;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 36; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||.||||||||

```
Db          3 TGCGTCGATGCAGGGGGG 20

RESULT 13
AAC80661
ID   AAC80661 standard; DNA; 20 BP.
XX
AC   AAC80661;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.
XX
KW   CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW   immunogenic; cytokine release; natural killer cell; NK cell activation;
KW   cell-mediated immune response; T-cell response; humoral response;
KW   B-cell response; antibody production; immune response induction; vaccine;
KW   allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW   parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW   rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW   immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW   antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW   antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200061151-A2.
XX
PD   19-OCT-2000.
XX
PF   12-APR-2000; 2000WO-US009839.
XX
PR   12-APR-1999;   99US-0128898P.
XX
PA   (KLIN/) KLINMAN D.
PA   (ISHI/) ISHII K.
PA   (VERT/) VERTHELYI D.
XX
PI   Klinman D,  Ishii K,  Verthelyi D;
XX
DR   WPI; 2001-006880/01.
XX
PT   Novel oligonucleotides useful for the prevention and treatment of
PT   allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT   resulting from exposure to a bio-warfare agent.
XX
PS   Claim 4; Page 36; 46pp; English.
XX
CC   The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC   (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC   comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC   -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC   optionally have phosphorothioate linkages which make them more resistant
CC   to degradation. The invention also relates to an oligonucleotide delivery
CC   complex comprising an oligonucleotide of the invention and a targetting
CC   agent, and a pharmaceutical composition comprising the oligonucleotide
CC   delivery complex. The oligonucleotides are able to induce either a cell-
CC   mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC   oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC   cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC   being able to induce a humoral response. It is thought that after
CC   administration, the oligonucleotide acts on antigen-presenting cells
CC   (e.g., macrophages and dendritic cells), which then release cytokines,
CC   leading to activation of natural killer (NK) cells. A cell-mediated or
CC   humoral response can then occur by activation of T- or B-cells. The
CC   induction of an immune response is useful for treating, preventing or
CC   ameliorating an allergic reaction (preferably asthma), or an infection,
CC   where an immunogenic CpG oligonucleotide is administered either alone or
CC   in combination with an anti-allergenic agent or anti-infectious agent.
CC   The allergic conditions which may be treated include eczema, allergic
CC   rhinitis, hayfever, urticaria, food allergies and other atopic
CC   conditions, and the infections which may be treated include viral,
CC   bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC   leishmania and schistosomiasis. Immune response induction may also be
CC   used in the treatment of an autoimmune disorder (e.g., lupus
CC   erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC   associated with immune system deficiency, and symptoms resulting from
CC   exposure to an agent of biological warfare. An immunogenic CpG
CC   oligonucleotide, either alone or in combination with an anti-cancer
CC   agent, is useful for treating solid tumour cancer. The induction of an
CC   immune response is used in antisense therapy and to improve the efficacy
CC   of a vaccine. The oligonucleotide is preferably administered to
CC   lymphocytes ex vivo, producing activated lymphocytes which are then
CC   administered to the host. The present sequence represents an immunogenic
CC   CpG oligodeoxynucleotide of the invention
XX
SQ   Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

  Query Match             91.1%;  Score 16.4;  DB 4;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 2.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              |||||||| |||||||||
Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 14
AAC80620
ID   AAC80620 standard; DNA; 20 BP.
XX
AC   AAC80620;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.
XX
KW   CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW   immunogenic; cytokine release; natural killer cell; NK cell activation;
KW   cell-mediated immune response; T-cell response; humoral response;
KW   B-cell response; antibody production; immune response induction; vaccine;
KW   allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW   parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW   rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW   immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW   antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW   antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200061151-A2.
XX
PD   19-OCT-2000.
XX
PF   12-APR-2000; 2000WO-US009839.
XX
PR   12-APR-1999;   99US-0128898P.
XX
PA   (KLIN/) KLINMAN D.
PA   (ISHI/) ISHII K.
PA   (VERT/) VERTHELYI D.
XX
PI   Klinman D,  Ishii K,  Verthelyi D;
XX
DR   WPI; 2001-006880/01.
XX
PT   Novel oligonucleotides useful for the prevention and treatment of
PT   allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT   resulting from exposure to a bio-warfare agent.
XX
PS   Claim 4; Page 30; 46pp; English.
XX
CC   The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC   (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC   comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC   -3'. The central CpG motif is unmethylated, and the oligonucleotides
```

CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

```
  Query Match             91.1%;  Score 16.4;  DB 4;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 2.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||  |||||||||
Db          3 TGCGTCGATGCAGGGGGG 20
```

RESULT 15
AAS09650
ID AAS09650 standard; DNA; 20 BP.
XX
AC AAS09650;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #100.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 43; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

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  Query Match             91.1%;  Score 16.4;  DB 4;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 2.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||| ||||||||||||||
Db          3 TGCATCGACGCAGGGGGG 20
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Search completed: April 29, 2005, 06:26:01
Job time : 184.527 secs

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1687.62 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-14
Perfect score: 18
Sequence: 1 tgcgtcgacgcaggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16.4	91.1	894	9	CG395429	ZMMBBc001
	2	16	88.9	443	2	BE453868	BE453868 946047E07
	3	16	88.9	469	2	BE510146	BE510146 946047E07
	4	16	88.9	469	8	BZ583033	BZ583033 3590_1_49
	5	16	88.9	481	3	AY106226	AY106226 Zea mays
c	6	16	88.9	488	9	CG305844	CG305844 OG0BX58TV
	7	16	88.9	498	5	BQ762616	BQ762616 EBro02_SQ
	8	16	88.9	502	4	BM428951	BM428951 952026C01
	9	16	88.9	512	4	BI779441	BI779441 EBro01_SQ
	10	16	88.9	541	9	CG305830	CG305830 OG0BX58TH
	11	16	88.9	562	5	BQ238846	BQ238846 TaE05040D
	12	16	88.9	573	5	BU499653	BU499653 946178A11
	13	16	88.9	600	5	BU049816	BU049816 1111015B0
	14	16	88.9	795	9	CG303497	CG303497 OG1AI84TH
c	15	16	88.9	939	5	BQ135709	BQ135709 NF010G08E
	16	16	88.9	970	9	CG299311	CG299311 OG2BJ70TV
	17	16	88.9	1032	9	CL987494	CL987494 ZMMBHe000
c	18	15.4	85.6	176	9	CE366192	CE366192 tigr-gss-
	19	15.4	85.6	241	1	AA807153	AA807153 oc36d11.s
	20	15.4	85.6	246	1	AV253772	AV253772 AV253772
	21	15.4	85.6	346	6	CD660132	CD660132 EtESTef31
	22	15.4	85.6	349	5	BU038662	BU038662 DH02G09 H
c	23	15.4	85.6	356	4	BG059197	BG059197 nah51e03.
c	24	15.4	85.6	382	4	BJ492497	BJ492497 BJ492497
c	25	15.4	85.6	467	8	AQ221882	AQ221882 HS_2240_A
	26	15.4	85.6	490	1	AA533540	AA533540 nj68f04.s
	27	15.4	85.6	496	2	AW265217	AW265217 xp81b08.x
	28	15.4	85.6	504	1	AI812904	AI812904 22C9 Pine
c	29	15.4	85.6	545	4	BI489134	BI489134 603021222
	30	15.4	85.6	569	6	CD666782	CD666782 EtESTeg30
	31	15.4	85.6	586	7	CV458196	CV458196 aof02-6ms
c	32	15.4	85.6	629	4	BJ496322	BJ496322 BJ496322
c	33	15.4	85.6	634	7	CF484481	CF484481 POL1_25_C
	34	15.4	85.6	642	8	CC133569	CC133569 NDL.94N20
c	35	15.4	85.6	657	4	BJ493235	BJ493235 BJ493235
c	36	15.4	85.6	663	4	BJ500451	BJ500451 BJ500451
	37	15.4	85.6	664	7	CV289422	CV289422 aof01-1ms
c	38	15.4	85.6	665	6	CA078334	CA078334 SCRLAM100
	39	15.4	85.6	673	4	BJ512362	BJ512362 BJ512362
c	40	15.4	85.6	680	6	CA290160	CA290160 SCAGFL801
	41	15.4	85.6	687	6	CD348840	CD348840 UI-M-FY0-
	42	15.4	85.6	712	9	CG440448	CG440448 OGVHG74TV
	43	15.4	85.6	717	4	BJ744446	BJ744446 BJ744446
c	44	15.4	85.6	723	4	BJ733562	BJ733562 BJ733562
c	45	15.4	85.6	748	6	CD794512	CD794512 EST665873

ALIGNMENTS

RESULT 1
CG395429/c
LOCUS CG395429 894 bp DNA linear GSS 22-SEP-2003
DEFINITION ZMMBBc0011O17r ZMMBBc (EcoRI) Zea mays genomic clone ZMMBBc0011O17 3', genomic survey sequence.
ACCESSION CG395429
VERSION CG395429.1 GI:34338654
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 894)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003b)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 64.
FEATURES Location/Qualifiers
source 1. .894
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBc0011O17"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 894;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||| ||||||||

```
Db        800 TGCGTCGACTCAGGGGGG 783


RESULT 2
BE453868
LOCUS       BE453868                443 bp    mRNA    linear   EST 26-JUL-2000
DEFINITION  946047E07.y1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE453868
VERSION     BE453868.1  GI:9461714
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946047  row: E  column: 07.
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 2;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        129 TGCGTCGACGCAGGGG 144


RESULT 3
BE510146
LOCUS       BE510146                469 bp    mRNA    linear   EST 07-AUG-2000
DEFINITION  946047E07.y2 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE510146
VERSION     BE510146.1  GI:9731394
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946047  row: E  column: 07.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 2;  Length 469;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        119 TGCGTCGACGCAGGGG 134


RESULT 4
BZ583033
LOCUS       BZ583033                469 bp    DNA     linear   GSS 17-DEC-2002
DEFINITION  3590_1_49_1_A01.y_1 3590 - RescueMu Grid M Zea mays genomic,
            genomic survey sequence.
ACCESSION   BZ583033
VERSION     BZ583033.1  GI:27218094
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 3590_1_49_1  column: 10
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
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/clone_lib="3590 - RescueMu Grid M"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid M was grown at University of Arizona in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
ORIGIN

Query Match 88.9%; Score 16; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGG 16
||||||||||||||||
Db 262 TGCGTCGACGCAGGGG 277

RESULT 5
AY106226
LOCUS AY106226 481 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PCO146698 mRNA sequence.
ACCESSION AY106226
VERSION AY106226.1 GI:21209304
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 481)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 481)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
source 1. .481
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:638670"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN

Query Match 88.9%; Score 16; DB 3; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGG 16
||||||||||||||||
Db 260 TGCGTCGACGCAGGGG 275

RESULT 6
CG305844/c
LOCUS CG305844 488 bp DNA linear GSS 25-AUG-2003
DEFINITION OG0BX58TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0683I20, genomic survey sequence.
ACCESSION CG305844
VERSION CG305844.1 GI:34220058
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 488)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OG0BX58TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .488
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMa0683I20"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"
ORIGIN

Query Match 88.9%; Score 16; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGG 16
||||||||||||||||
Db 213 TGCGTCGACGCAGGGG 198

RESULT 7
BQ762616
LOCUS BQ762616 498 bp mRNA linear EST 26-JUL-2002
DEFINITION EBro02_SQ004_A16_R root, 3 week, hydroponic grown, low nitrogen, cv Optic, EBro02 Hordeum vulgare subsp. vulgare cDNA clone EBro02_SQ004_A16 5', mRNA sequence.
ACCESSION BQ762616
VERSION BQ762616.1 GI:21971088
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 498)
AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources

```
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .498
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Optic"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="EBro02_SQ004_A16"
                     /tissue_type="root"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="root, 3 week, hydroponic grown, low nitrogen,
                     cv Optic, EBro02"
                     /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
                     Non-normalised library, directionally cloned into pSPORT1.
                     Derived from roots of 3 week old Nitrogen stressed barley
                     plants. Developed as part of the barley transcriptome
                     resources of BBSRC/SEERAD funded cereal IGF (Investigating
                     Gene Function) project."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 5;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGTCGACGCAGGGGGG 18
              ||||||||||||||||
Db        405 CGTCGACGCAGGGGGG 420


RESULT 8
BM428951
LOCUS       BM428951                 502 bp    mRNA    linear   EST 31-JAN-2002
DEFINITION  952026C01.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
            mays cDNA, mRNA sequence.
ACCESSION   BM428951
VERSION     BM428951.1  GI:18450673
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 952026  row: C  column: 01.
FEATURES             Location/Qualifiers
     source          1. .502
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="BMS (Black Mexican Sweet)"
                     /db_xref="taxon:4577"
                     /tissue_type="suspension culture"
                     /dev_stage="mixed logarithmic and stationary growth
                     phases"
                     /lab_host="DH10B"
                     /clone_lib="952 - BMS tissue from Walbot Lab (reduced
                     rRNA)"
                     /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The
                     library was prepared by George Rudenko using poly (A)
                     selected RNA and Universal Riboclone cDNA Synthesis System
                     (Promega). cDNA was synthesized using both random and
                     oligo(dT) primers in separate reactions and equipped with
                     EcoRI adaptors. Library was size-fractionated on agarose
                     gels (for insert size >400bp) and non-directionally cloned
                     into EcoRI-digested pUC19 vector. Blue/white selection on
                     carbenicillin-containing plates was used to recover
                     positive clones."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        182 TGCGTCGACGCAGGGG 197


RESULT 9
BI779441
LOCUS       BI779441                 512 bp    mRNA    linear   EST 23-JUL-2002
DEFINITION  EBro01_SQ004_A20_R root, 3 week, hydroponic grown, no treatment, cv
            Optic, EBro01 Hordeum vulgare subsp. vulgare cDNA clone
            EBro01_SQ004_A20 5', mRNA sequence.
ACCESSION   BI779441
VERSION     BI779441.2  GI:21947112
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
            Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
  TITLE     Development of Barley Transcriptome Resources
  JOURNAL   Unpublished (2001)
COMMENT     On Sep 26, 2001 this sequence version replaced gi:15782333.
            Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk
            All sequence has a Phred quality score of 20 or over
            Seq primer: M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Optic"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="EBro01_SQ004_A20"
                     /tissue_type="root"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="root, 3 week, hydroponic grown, no treatment,
                     cv Optic, EBro01"
                     /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
                     Non-normalised library, directionally cloned into pSPORT1.
                     Derived from roots of 3 week old hydroponically grown
                     unstressed barley plants.  Developed as part of the barley
                     transcriptome resources of BBSRC/SEERAD funded cereal IGF
                     (Investigating Gene Function) project."
ORIGIN
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  Query Match             88.9%;  Score 16;  DB 4;  Length 512;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGTCGACGCAGGGGGG 18
              ||||||||||||||||
Db        407 CGTCGACGCAGGGGGG 422


RESULT 10
CG305830
LOCUS       CG305830                 541 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG0BX58TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0683I20,
            genomic survey sequence.
ACCESSION   CG305830
VERSION     CG305830.1  GI:34220044
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG0BX58TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .541
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0683I20"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 9;  Length 541;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        276 TGCGTCGACGCAGGGG 291


RESULT 11
BQ238846
LOCUS       BQ238846                 562 bp    mRNA    linear   EST 03-MAY-2002
DEFINITION  TaE05040D12R TaE05 Triticum aestivum cDNA clone TaE05040D12R, mRNA
            sequence.
ACCESSION   BQ238846
VERSION     BQ238846.1  GI:20434722
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Cloutier,S.
  TITLE     Wheat functional genomics - Glenlea developing seeds cDNA libraries
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Dr. Sylvie Cloutier
            Cereal Research Centre, Agriculture and Agri-food Canada
            195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
            Tel: (204) 983-2340
            Fax: (204) 983-4604
            Email: scloutier@agr.gc.ca
            was cloned directionally, not all sequences generated with reverse
            primer were from the 5' end (same with forward primer and 3' end).
            Average insert size is >2.0 kb
            Plate: 040  row: D  column: 12
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .562
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Glenlea"
                     /db_xref="taxon:4565"
                     /clone="TaE05040D12R"
                     /tissue_type="developing seeds"
                     /dev_stage="5 days after anthesis"
                     /lab_host="E. coli DH10B"
                     /clone_lib="TaE05"
                     /note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
                     NotI; Site_2: MluI; mRNA obtained from wheat seeds of
                     cultivar Glenlea 5 days post-anthesis"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 5;  Length 562;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGTCGACGCAGGGGGG 18
              ||||||||||||||||
Db        441 CGTCGACGCAGGGGGG 456


RESULT 12
BU499653
LOCUS       BU499653                 573 bp    mRNA    linear   EST 12-SEP-2002
DEFINITION  946178A11.y1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BU499653
VERSION     BU499653.1  GI:22819563
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946178  row: A  column: 11.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
```

```
                    inflorescence development"
                    /lab_host="XLOLR"
                    /clone_lib="946 - tassel primordium prepared by Schmidt
                    lab"
                    /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                    Site_2: XhoI; George Chuck dissected immature tassels
                    between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                    library in HybriZAP.  Sample insert size  range was 350 bp
                    to 3 Kb with a 1 Kb average."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 5;  Length 573;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        142 TGCGTCGACGCAGGGG 157


RESULT 13
BU049816
LOCUS       BU049816                600 bp    mRNA    linear   EST 26-AUG-2002
DEFINITION  1111015B03.y1 1111 - Unigene III from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   BU049816
VERSION     BU049816.1  GI:22489893
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1111015  row: B  column: 03.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="dbEST:952026C01.y1"
                     /db_xref="taxon:4577"
                     /clone_lib="1111 - Unigene III from Maize Genome Project"
                     /note="This library represents the unique genes found in
                     the third round of EST sequencing at Stanford University
                     for the maize genome project. Sequences are present from
                     library 952. Contigs were assembled using ZmDBAssembler
                     and 2 representatives from each contig were selected for
                     the Unigene set. All singlets were also selected."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 5;  Length 600;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        176 TGCGTCGACGCAGGGG 191


RESULT 14
CG303497
LOCUS       CG303497                795 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG1AI84TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0717M23,
            genomic survey sequence.
ACCESSION   CG303497
VERSION     CG303497.1  GI:34217711
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG1AI84TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0717M23"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 9;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        337 TGCGTCGACGCAGGGG 352


RESULT 15
BQ135709/c
LOCUS       BQ135709                939 bp    mRNA    linear   EST 23-APR-2002
DEFINITION  NF010G08EC1F1068 Elicited cell culture Medicago truncatula cDNA
            clone NF010G08EC 5', mRNA sequence.
ACCESSION   BQ135709
VERSION     BQ135709.1  GI:20271833
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
            Center for Medicago Genomics Research
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Dixon RA
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7302
            Fax: 580 221 7380
            Email: radixon@noble.org
```

```
            Insert Length: 939   Std Error: 0.00
            Plate: 010  row: G  column: 08
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES              Location/Qualifiers
     source           1. .939
                      /organism="Medicago truncatula"
                      /mol_type="mRNA"
                      /db_xref="taxon:3880"
                      /clone="NF010G08EC"
                      /tissue_type="Cell cultures derived from root tissues"
                      /dev_stage="Cell suspensions were subcultured every 14
                      days. Cells were induced six days after subculture"
                      /clone_lib="Elicited cell culture"
                      /note="Vector: Lambda Zap; Cells were induced with yeast
                      cell wall extracts equivalent to  50ug/ml glucose in the
                      final concentration. Samples were taken at  0.5, 1, 12 and
                      24 hours after induction. Equal amounts of RNA from  each
                      time point were pooled and used for mRNA isolation."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 5;  Length 939;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              ||||||||||||||||
Db        824 TGCGTCGACGCAGGGG 809


Search completed: April 29, 2005, 11:55:21
Job time : 1691.62 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 52.6622 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-14
Perfect score: 18
Sequence: 1 tgcgtcgacgcaggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.8	82.2	601	4	US-09-949-016-19321	Sequence 19321, A
	2	14.8	82.2	601	4	US-09-949-016-19322	Sequence 19322, A
	3	14.8	82.2	601	4	US-09-949-016-62925	Sequence 62925, A
	4	14.8	82.2	601	4	US-09-949-016-62926	Sequence 62926, A
c	5	14.8	82.2	9818	4	US-09-902-540-987	Sequence 987, App
	6	14.8	82.2	17020	4	US-09-949-016-11818	Sequence 11818, A
	7	14.8	82.2	17021	4	US-09-949-016-13555	Sequence 13555, A
	8	14.8	82.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	9	14.8	82.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	10	14.4	80.0	879	4	US-09-902-540-3692	Sequence 3692, Ap
c	11	14.4	80.0	996	4	US-09-252-991A-11818	Sequence 11818, A
c	12	14.4	80.0	1275	4	US-09-252-991A-251	Sequence 251, App
	13	14.4	80.0	1545	4	US-09-252-991A-11565	Sequence 11565, A
	14	14.4	80.0	1584	4	US-09-489-039A-2524	Sequence 2524, Ap
	15	14.4	80.0	1785	4	US-09-252-991A-281	Sequence 281, App
c	16	14.4	80.0	2589	4	US-09-252-991A-11884	Sequence 11884, A
	17	14.4	80.0	18195	4	US-09-902-540-1179	Sequence 1179, Ap
c	18	14	77.8	19	3	US-08-943-731-596	Sequence 596, App
c	19	14	77.8	1817	3	US-08-943-731-193	Sequence 193, App
c	20	14	77.8	20084	3	US-08-943-731-5	Sequence 5, Appli
	21	13.8	76.7	348	4	US-09-902-540-8168	Sequence 8168, Ap
	22	13.8	76.7	352	4	US-09-640-211A-1457	Sequence 1457, Ap
c	23	13.8	76.7	594	4	US-09-489-039A-7023	Sequence 7023, Ap
	24	13.8	76.7	693	4	US-09-902-540-8551	Sequence 8551, Ap
c	25	13.8	76.7	906	4	US-09-489-039A-1946	Sequence 1946, Ap
	26	13.8	76.7	921	4	US-09-902-540-8318	Sequence 8318, Ap
c	27	13.8	76.7	973	4	US-09-482-273-13	Sequence 13, Appl
c	28	13.8	76.7	984	4	US-09-482-273-82	Sequence 82, Appl
c	29	13.8	76.7	1074	4	US-09-252-991A-5833	Sequence 5833, Ap
c	30	13.8	76.7	1110	4	US-09-252-991A-8962	Sequence 8962, Ap
c	31	13.8	76.7	1188	4	US-09-902-540-9280	Sequence 9280, Ap
	32	13.8	76.7	1278	4	US-09-252-991A-9043	Sequence 9043, Ap
	33	13.8	76.7	1336	4	US-09-902-540-1945	Sequence 1945, Ap
	34	13.8	76.7	1554	4	US-09-252-991A-5777	Sequence 5777, Ap
	35	13.8	76.7	1818	3	US-09-221-017B-792	Sequence 792, App
c	36	13.8	76.7	1905	4	US-09-902-540-6144	Sequence 6144, Ap
	37	13.8	76.7	1947	4	US-09-902-540-6780	Sequence 6780, Ap
c	38	13.8	76.7	1968	4	US-09-252-991A-8743	Sequence 8743, Ap
	39	13.8	76.7	2203	4	US-09-902-540-4252	Sequence 4252, Ap
c	40	13.8	76.7	2656	4	US-09-902-540-295	Sequence 295, App
c	41	13.8	76.7	3653	4	US-09-902-540-555	Sequence 555, App
c	42	13.8	76.7	3704	4	US-10-160-719A-57	Sequence 57, Appl
	43	13.8	76.7	7103	4	US-09-949-016-16711	Sequence 16711, A
c	44	13.8	76.7	7562	4	US-09-902-540-902	Sequence 902, App
c	45	13.8	76.7	8048	4	US-09-902-540-867	Sequence 867, App

ALIGNMENTS

RESULT 1
US-09-949-016-19321
; Sequence 19321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19321
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-19321

Query Match 82.2%; Score 14.8; DB 4; Length 601;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||| ||||||||| ||
Db        257 TGCGTAGACGCAGGGAGG 274
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RESULT 2
US-09-949-016-19322
; Sequence 19322, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19322
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-19322

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||| |||||||||| ||
Db         33 TGCGTAGACGCAGGGAGG 50


RESULT 3
US-09-949-016-62925
; Sequence 62925, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62925
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-62925

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||| |||||||||| ||
Db        257 TGCGTAGACGCAGGGAGG 274


RESULT 4
US-09-949-016-62926
; Sequence 62926, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62926
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-62926

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 601;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||| |||||||||| ||
Db         33 TGCGTAGACGCAGGGAGG 50


RESULT 5
US-09-902-540-987/c
; Sequence 987, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 987
;    LENGTH: 9818
;    TYPE: DNA
;    ORGANISM: Myxococcus xanthus
US-09-902-540-987

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 9818;
  Best Local Similarity   88.9%;  Pred. No. 3.9e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              || |||||||||| ||||
Db       8555 TGGGTCGACGCAGAGGGG 8538


RESULT 6
US-09-949-016-11818
; Sequence 11818, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11818
;    LENGTH: 17020
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-11818

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 17020;
  Best Local Similarity   88.9%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||| |||||||||| ||
Db       7290 TGCGTAGACGCAGGGAGG 7307


RESULT 7
US-09-949-016-13555
; Sequence 13555, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13555
;   LENGTH: 17021
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13555

  Query Match             82.2%;  Score 14.8;  DB 4;  Length 17021;
  Best Local Similarity   88.9%;  Pred. No. 3.8e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||| |||||||||| ||
Db       7290 TGCGTAGACGCAGGGAGG 7307


RESULT 8
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             82.2%;  Score 14.8;  DB 3;  Length 4403765;
  Best Local Similarity   88.9%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              |||||||||| || |||
Db    3717044 TGCGTCGACGCTGGCGGG 3717061


RESULT 9
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             82.2%;  Score 14.8;  DB 3;  Length 4411529;
  Best Local Similarity   88.9%;  Pred. No. 2e+02;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              |||||||||| || |||
Db    3719484 TGCGTCGACGCTGGCGGG 3719501


RESULT 10
US-09-902-540-3692
; Sequence 3692, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3692
;   LENGTH: 879
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-3692

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 879;
  Best Local Similarity   93.8%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGG 16
              |||| ||||||||||
Db        480 TGCGGCGACGCAGGGG 495


RESULT 11
US-09-252-991A-11818/c
; Sequence 11818, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
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;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11818
;   LENGTH: 996
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11818

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 996;
  Best Local Similarity   93.8%;  Pred. No. 7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGTCGACGCAGGGGG 17
              ||||||||||||| ||
Db        963 GCGTCGACGCAGGCGG 948


RESULT 12
US-09-252-991A-251/c
; Sequence 251, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 251
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-251

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1275;
  Best Local Similarity   93.8%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGTCGACGCAGGGGG 17
              |||||||||||| |||
Db        200 GCGTCGACGCAGTGGG 185


RESULT 13
US-09-252-991A-11565
; Sequence 11565, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11565
;   LENGTH: 1545
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11565

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1545;
  Best Local Similarity   93.8%;  Pred. No. 6.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGTCGACGCAGGGGG 17
              |||||||||||| ||
Db        611 GCGTCGACGCAGGCGG 626


RESULT 14
US-09-489-039A-2524
; Sequence 2524, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 2524
;   LENGTH: 1584
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2524

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1584;
  Best Local Similarity   93.8%;  Pred. No. 6.8e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGTCGACGCAGGGGG 17
              |||||| |||||||||
Db       1057 GCGTCGGCGCAGGGGG 1072


RESULT 15
US-09-252-991A-281
; Sequence 281, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 281
;   LENGTH: 1785
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-281

  Query Match             80.0%;  Score 14.4;  DB 4;  Length 1785;
  Best Local Similarity   93.8%;  Pred. No. 6.7e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGTCGACGCAGGGGG 17
              |||||||||||| |||
Db       1322 GCGTCGACGCAGTGGG 1337


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Job time : 64.7872 secs
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OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 241.419 Seconds
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Title: US-10-068-160A-14
Perfect score: 18
Sequence: 1 tgcgtcgacgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	14	US-10-068-160-14	Sequence 14, Appl
2	18	100.0	20	14	US-10-068-160-31	Sequence 31, Appl
3	18	100.0	20	15	US-10-194-035-39	Sequence 39, Appl
4	18	100.0	20	15	US-10-194-035-41	Sequence 41, Appl
5	18	100.0	20	18	US-10-666-022-3	Sequence 3, Appli
6	18	100.0	20	18	US-10-486-755-7	Sequence 7, Appli
7	18	100.0	20	18	US-10-486-755-21	Sequence 21, Appl
8	18	100.0	20	19	US-10-499-597-19	Sequence 19, Appl
9	16.4	91.1	18	14	US-10-068-160-16	Sequence 16, Appl
10	16.4	91.1	18	14	US-10-068-160-19	Sequence 19, Appl
11	16.4	91.1	20	11	US-09-874-991C-498	Sequence 498, App
12	16.4	91.1	20	11	US-09-874-991C-509	Sequence 509, App
13	16.4	91.1	20	11	US-09-874-991C-542	Sequence 542, App
14	16.4	91.1	20	14	US-10-068-160-7	Sequence 7, Appli
15	16.4	91.1	20	14	US-10-068-160-35	Sequence 35, Appl
16	16.4	91.1	20	15	US-10-194-035-40	Sequence 40, Appl
17	16.4	91.1	20	15	US-10-194-035-81	Sequence 81, Appl
18	16.4	91.1	20	15	US-10-194-035-82	Sequence 82, Appl
19	16.4	91.1	20	15	US-10-194-035-100	Sequence 100, App
20	16.4	91.1	20	18	US-10-666-022-4	Sequence 4, Appli
21	16.4	91.1	20	18	US-10-666-022-7	Sequence 7, Appli
22	16.4	91.1	20	18	US-10-666-022-16	Sequence 16, Appl
23	16.4	91.1	20	18	US-10-486-755-4	Sequence 4, Appli
24	16.4	91.1	20	18	US-10-486-755-10	Sequence 10, Appl
25	16.4	91.1	20	18	US-10-486-755-13	Sequence 13, Appl
26	16.4	91.1	20	18	US-10-486-755-18	Sequence 18, Appl
27	16.4	91.1	20	18	US-10-486-755-20	Sequence 20, Appl
28	16.4	91.1	20	18	US-10-486-755-25	Sequence 25, Appl
29	16.4	91.1	20	19	US-10-499-597-14	Sequence 14, Appl
30	16.4	91.1	20	19	US-10-499-597-21	Sequence 21, Appl
31	16.4	91.1	28	11	US-09-874-991C-519	Sequence 519, App
32	16.4	91.1	28	11	US-09-874-991C-531	Sequence 531, App
c 33	16.4	91.1	512	18	US-10-425-115-155944	Sequence 155944,
c 34	16.4	91.1	34115	18	US-10-739-096-34	Sequence 34, Appl
c 35	16.4	91.1	34115	19	US-10-494-364-34	Sequence 34, Appl
36	16	88.9	1272	17	US-10-425-114-24809	Sequence 24809, A
37	16	88.9	1836	18	US-10-425-115-167520	Sequence 167520,
38	15.4	85.6	19	15	US-10-194-035-83	Sequence 83, Appl
39	15.4	85.6	19	15	US-10-194-035-88	Sequence 88, Appl
c 40	15.4	85.6	437	18	US-10-425-115-167975	Sequence 167975,
c 41	15.4	85.6	1752	18	US-10-437-963-45085	Sequence 45085, A
c 42	15.4	85.6	2661	18	US-10-437-963-42293	Sequence 42293, A
c 43	15.4	85.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
44	15	83.3	512	17	US-10-260-238-4621	Sequence 4621, Ap
c 45	15	83.3	568	9	US-09-764-877-956	Sequence 956, App

ALIGNMENTS

RESULT 1
US-10-068-160-14
; Sequence 14, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-14

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          1 TGCGTCGACGCAGGGGGG 18
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RESULT 2
US-10-068-160-31
; Sequence 31, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-31

  Query Match             100.0%;  Score 18;  DB 14;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 3
US-10-194-035-39
; Sequence 39, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-39

  Query Match             100.0%;  Score 18;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 4
US-10-194-035-41
; Sequence 41, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-41

  Query Match             100.0%;  Score 18;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 5
US-10-666-022-3
; Sequence 3, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISE
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(20)
;   OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-3

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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```
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 6
US-10-486-755-7
; Sequence 7, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG oligodeoxynucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: n is any base, or is no base at all
US-10-486-755-7

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 7
US-10-486-755-21
; Sequence 21, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-486-755-21

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 8
US-10-499-597-19
; Sequence 19, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Rouse, Barry T.
;  APPLICANT:  Zheng, Mei
;  TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
;  FILE REFERENCE: 4239-64125-02
;  CURRENT APPLICATION NUMBER: US/10/499,597
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: PCT/US02/40955
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,457
;  PRIOR FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG D oligonucleotide
US-10-499-597-19

  Query Match             100.0%;  Score 18;  DB 19;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGTCGACGCAGGGGGG 20


RESULT 9
US-10-068-160-16
; Sequence 16, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-16
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Query Match 91.1%; Score 16.4; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||||||||| |||||||||
Db 1 TGCGTCGATGCAGGGGGG 18

RESULT 10
US-10-068-160-19
; Sequence 19, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-19

Query Match 91.1%; Score 16.4; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||| |||||||||||||
Db 1 TGCATCGACGCAGGGGGG 18

RESULT 11
US-09-874-991C-498
; Sequence 498, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-498

Query Match 91.1%; Score 16.4; DB 11; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||| |||||||||||||
Db 3 TGCATCGACGCAGGGGGG 20

RESULT 12
US-09-874-991C-509
; Sequence 509, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-509

Query Match 91.1%; Score 16.4; DB 11; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
||| |||||||||||||
Db 3 TGCATCGACGCAGGGGGG 20

RESULT 13
US-09-874-991C-542
; Sequence 542, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-542

Query Match 91.1%; Score 16.4; DB 11; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGTCGACGCAGGGGGG 18
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Db 3 TGCATCGACGCAGGGGGG 20

RESULT 14
US-10-068-160-7
; Sequence 7, Application US/10068160

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; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

  Query Match             91.1%;  Score 16.4;  DB 14;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
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Db          3 TGCGTCGATGCAGGGGGG 20


RESULT 15
US-10-068-160-35
; Sequence 35, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-35

  Query Match             91.1%;  Score 16.4;  DB 14;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.6e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGTCGACGCAGGGGGG 18
              ||| ||||||||||||||
Db          3 TGCATCGACGCAGGGGGG 20


Search completed: April 29, 2005, 12:35:46
Job time : 246.419 secs
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الأهرام (مصر)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 241.419 Seconds
(without alignments)
453.893 Million cell updates/sec

Title: US-10-068-160A-17
Perfect score: 18
Sequence: 1 tgcgccggcgcagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	14	US-10-068-160-17	Sequence 17, Appl
	2	18	100.0	20	18	US-10-666-022-5	Sequence 5, Appli
	3	18	100.0	20	18	US-10-486-755-8	Sequence 8, Appli
c	4	16.4	91.1	687	18	US-10-437-963-58926	Sequence 58926, A
	5	16.4	91.1	96256	18	US-10-775-169-352	Sequence 352, App
c	6	16	88.9	654	18	US-10-767-701-4709	Sequence 4709, Ap
c	7	16	88.9	2052	18	US-10-437-963-55777	Sequence 55777, A
	8	15.4	85.6	224	18	US-10-425-115-101101	Sequence 101101,
c	9	15.4	85.6	250	18	US-10-425-115-51314	Sequence 51314, A
c	10	15.4	85.6	264	18	US-10-425-115-165902	Sequence 165902,
c	11	15.4	85.6	369	18	US-10-437-963-3377	Sequence 3377, Ap
c	12	15.4	85.6	373	18	US-10-767-701-19238	Sequence 19238, A
c	13	15.4	85.6	437	18	US-10-425-115-167975	Sequence 167975,
	14	15.4	85.6	480	18	US-10-425-115-166714	Sequence 166714,
c	15	15.4	85.6	483	17	US-10-425-114-14407	Sequence 14407, A
	16	15.4	85.6	492	18	US-10-425-115-161395	Sequence 161395,
c	17	15.4	85.6	513	14	US-10-198-846-1956	Sequence 1956, Ap
c	18	15.4	85.6	564	18	US-10-430-201-1699	Sequence 1699, Ap
c	19	15.4	85.6	564	18	US-10-430-201-1700	Sequence 1700, Ap
c	20	15.4	85.6	573	18	US-10-437-963-79096	Sequence 79096, A
c	21	15.4	85.6	581	18	US-10-425-115-84131	Sequence 84131, A
c	22	15.4	85.6	597	16	US-10-029-386-4446	Sequence 4446, Ap
	23	15.4	85.6	611	18	US-10-425-115-51672	Sequence 51672, A
c	24	15.4	85.6	614	18	US-10-425-115-177315	Sequence 177315,
	25	15.4	85.6	616	18	US-10-437-963-22077	Sequence 22077, A
	26	15.4	85.6	638	18	US-10-425-115-58066	Sequence 58066, A
c	27	15.4	85.6	644	18	US-10-767-701-22730	Sequence 22730, A
c	28	15.4	85.6	664	14	US-10-198-846-7873	Sequence 7873, Ap
c	29	15.4	85.6	681	15	US-10-259-165-431	Sequence 431, App
c	30	15.4	85.6	684	15	US-10-259-165-99	Sequence 99, Appl
c	31	15.4	85.6	745	14	US-10-198-846-11115	Sequence 11115, A
	32	15.4	85.6	761	18	US-10-767-701-683	Sequence 683, App
	33	15.4	85.6	785	17	US-10-425-114-2950	Sequence 2950, Ap
c	34	15.4	85.6	792	18	US-10-767-701-8898	Sequence 8898, Ap
	35	15.4	85.6	804	17	US-10-369-493-41635	Sequence 41635, A
c	36	15.4	85.6	807	18	US-10-437-963-94871	Sequence 94871, A
c	37	15.4	85.6	813	18	US-10-767-701-7327	Sequence 7327, Ap
c	38	15.4	85.6	837	18	US-10-437-963-21218	Sequence 21218, A
c	39	15.4	85.6	900	14	US-10-101-464A-282	Sequence 282, App
c	40	15.4	85.6	900	19	US-10-864-252-282	Sequence 282, App
	41	15.4	85.6	929	17	US-10-425-114-21530	Sequence 21530, A
c	42	15.4	85.6	951	18	US-10-437-963-72702	Sequence 72702, A
	43	15.4	85.6	965	17	US-10-425-114-29232	Sequence 29232, A
c	44	15.4	85.6	1008	18	US-10-856-499-329	Sequence 329, App
	45	15.4	85.6	1091	18	US-10-425-115-78693	Sequence 78693, A

ALIGNMENTS

RESULT 1
US-10-068-160-17
; Sequence 17, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-17

Query Match 100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db          1 TGCGCCGGCGCAGGGGGG 18
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RESULT 2
US-10-666-022-5
; Sequence 5, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(20)
;   OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-5

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 99;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db          3 TGCGCCGGCGCAGGGGGG 20


RESULT 3
US-10-486-755-8
; Sequence 8, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
;  APPLICANT:  REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
;  APPLICANT:  HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Gursel, Mayda
;  APPLICANT:  Verhelyi, Daniela
;  TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
;  FILE REFERENCE: 4239-67746
;  CURRENT APPLICATION NUMBER: US/10/486,755
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: US 60/312,190
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: PCT/US02/25732
;  PRIOR FILING DATE: 2002-08-13
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG oligodeoxynucleotide
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: n is any base, or is no base at all
US-10-486-755-8

  Query Match             100.0%;  Score 18;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 99;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||||||||||||||
Db          3 TGCGCCGGCGCAGGGGGG 20


RESULT 4
US-10-437-963-58926/c
; Sequence 58926, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 58926
;   LENGTH: 687
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_60597C.1
US-10-437-963-58926

  Query Match             91.1%;  Score 16.4;  DB 18;  Length 687;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||||||||||||| |
Db        204 TGCGCCGGCGCAGGGGAG 187


RESULT 5
US-10-775-169-352
; Sequence 352, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Burczynski, Michael
;  APPLICANT:  Twine, Natalie
;  APPLICANT:  Dorner, Andrew
;  APPLICANT:  Trepicchio, William
;  TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
;  FILE REFERENCE: AM101080 (031896-013000)
;  CURRENT APPLICATION NUMBER: US/10/775,169
;  CURRENT FILING DATE:  2004-02-11
;  NUMBER OF SEQ ID NOS: 5278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352
;   LENGTH: 96256
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-775-169-352

  Query Match             91.1%;  Score 16.4;  DB 18;  Length 96256;
  Best Local Similarity   94.4%;  Pred. No. 47;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db      21755 TCCGCCGGCGCAGGGGGG 21772


RESULT 6
US-10-767-701-4709/c
; Sequence 4709, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4709
;   LENGTH: 654
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS86387_1
US-10-767-701-4709

  Query Match             88.9%;  Score 16;  DB 18;  Length 654;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGG 17
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Db        148 GCGCCGGCGCAGGGGG 133


RESULT 7
US-10-437-963-55777/c
; Sequence 55777, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 55777
;   LENGTH: 2052
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_57751C.1
US-10-437-963-55777

  Query Match             88.9%;  Score 16;  DB 18;  Length 2052;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGG 17
              ||||||||||||||||
Db        272 GCGCCGGCGCAGGGGG 257


RESULT 8
US-10-425-115-101101
; Sequence 101101, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 101101
;   LENGTH: 224
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_23717C.1
US-10-425-115-101101

  Query Match             85.6%;  Score 15.4;  DB 18;  Length 224;
  Best Local Similarity   94.1%;  Pred. No. 7.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGG 17
              ||||||||||||||| |
Db        202 TGCGCCGGCGCAGGGAG 218


RESULT 9
US-10-425-115-51314/c
; Sequence 51314, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 51314
;   LENGTH: 250
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(250)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_146796C.1
US-10-425-115-51314

  Query Match             85.6%;  Score 15.4;  DB 18;  Length 250;
  Best Local Similarity   94.1%;  Pred. No. 7.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||||||| |||
Db         34 GCGCCGGCGCAGGAGGG 18


RESULT 10
US-10-425-115-165902/c
; Sequence 165902, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
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;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 165902
;   LENGTH: 264
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(264)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_82887C.1
US-10-425-115-165902

  Query Match            85.6%;  Score 15.4;  DB 18;  Length 264;
  Best Local Similarity   94.1%;  Pred. No. 7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||||| |||||||
Db        152 GCGCCGGCGAAGGGGGG 136


RESULT 11
US-10-437-963-3377/c
; Sequence 3377, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3377
;   LENGTH: 369
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_10359C.1
US-10-437-963-3377

  Query Match            85.6%;  Score 15.4;  DB 18;  Length 369;
  Best Local Similarity   94.1%;  Pred. No. 6.4e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||| |||||
Db        280 GCGCCGGCGCACGGGGG 264


RESULT 12
US-10-767-701-19238/c
; Sequence 19238, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 19238
;   LENGTH: 373
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3480-033-P1-K1-F6
US-10-767-701-19238

  Query Match            85.6%;  Score 15.4;  DB 18;  Length 373;
  Best Local Similarity   94.1%;  Pred. No. 6.3e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGG 17
              ||||||||||||||| |
Db        280 TGCGCCGGCGCAGGGTG 264


RESULT 13
US-10-425-115-167975/c
; Sequence 167975, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 167975
;   LENGTH: 437
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(437)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_84775C.1
US-10-425-115-167975

  Query Match            85.6%;  Score 15.4;  DB 18;  Length 437;
  Best Local Similarity   94.1%;  Pred. No. 6.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||| ||||||||||
Db        160 GCGCCGACGCAGGGGGG 144


RESULT 14
US-10-425-115-166714
; Sequence 166714, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
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; SEQ ID NO 166714
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83621C.1
US-10-425-115-166714

Query Match 85.6%; Score 15.4; DB 18; Length 480;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||||||| ||||
Db        115 GCGCCGGCGCAGCGGGG 131
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RESULT 15
US-10-425-114-14407/c
; Sequence 14407, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14407
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB189-016-H8_FLI
US-10-425-114-14407

Query Match 85.6%; Score 15.4; DB 17; Length 483;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 GCGCCGGCGCAGGGGGG 18
              |||| |||||||||||||
Db        106 GCGCAGGCGCAGGGGGG 90
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Search completed: April 29, 2005, 12:35:47
Job time : 242.419 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 712.216 Seconds
(without alignments)
1224.620 Million cell updates/sec

Title: US-10-068-160A-17
Perfect score: 18
Sequence: 1 tgcgccggcgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	17	94.4	1405	14	SHE581560	AJ581560 Suid herp
c	2	17	94.4	232176	2	AC144804	AC144804 Gallus ga
c	3	16.4	91.1	448	6	AR496235	AR496235 Sequence
c	4	16.4	91.1	448	6	AR511517	AR511517 Sequence
c	5	16.4	91.1	616	8	AK122136	AK122136 Oryza sat
c	6	16.4	91.1	1665	8	AK060251	AK060251 Oryza sat
	7	16.4	91.1	4225	10	AB017578S1	AB017578 Rattus no
c	8	16.4	91.1	4898	1	AY422718	AY422718 Pseudomon
c	9	16.4	91.1	5278	1	AB004065	AB004065 Pseudomon
	10	16.4	91.1	34503	2	AC151612	AC151612 Emiliania
	11	16.4	91.1	96256	6	CQ861719	CQ861719 Sequence
	12	16.4	91.1	96256	9	HS117715	AL022315 Human DNA
	13	16.4	91.1	98359	2	AC149892	AC149892 Xenopus t
	14	16.4	91.1	106117	9	AC103564	AC103564 Homo sapi
c	15	16.4	91.1	155303	8	AP005064	AP005064 Oryza sat
	16	16.4	91.1	161617	9	AC093724	AC093724 Homo sapi
c	17	16.4	91.1	182944	2	AC133783	AC133783 Homo sapi
c	18	16.4	91.1	202612	2	AC148952	AC148952 Otolemur
c	19	16.4	91.1	235115	2	AC133256	AC133256 Rattus no
c	20	16.4	91.1	235785	2	AC121480	AC121480 Rattus no
	21	16.4	91.1	301399	1	AE017233	AE017233 Mycobacte
c	22	16	88.9	10029	1	AE008002	AE008002 Agrobacte
c	23	16	88.9	10029	1	AE009036	AE009036 Agrobacte
	24	16	88.9	14952	1	SMAJ4445	AJ224445 Sinorhizo
c	25	16	88.9	134940	2	AC018939	AC018939 Homo sapi
c	26	16	88.9	147984	2	AC141987	AC141987 Rattus no
	27	16	88.9	176150	8	AC135864	AC135864 Oryza sat
	28	16	88.9	300000	1	SME591784	AL591784 Sinorhizo
c	29	15.4	85.6	307	14	AB113311	AB113311 Hepatitis
c	30	15.4	85.6	307	14	AB113312	AB113312 Hepatitis
	31	15.4	85.6	353	11	BV191370	BV191370 sqnm17044
c	32	15.4	85.6	374	6	CQ418035	CQ418035 Sequence
c	33	15.4	85.6	450	6	CQ425116	CQ425116 Sequence
	34	15.4	85.6	744	8	BT014884	BT014884 Arabidops
c	35	15.4	85.6	852	11	PM3H12G	AL685751 Penicilli
	36	15.4	85.6	885	8	BT005764	BT005764 Arabidops
	37	15.4	85.6	887	8	AK107743	AK107743 Oryza sat
c	38	15.4	85.6	900	6	BD267140	BD267140 Compositi
c	39	15.4	85.6	900	6	AR566661	AR566661 Sequence
c	40	15.4	85.6	969	6	AX654633	AX654633 Sequence
	41	15.4	85.6	976	11	PM12D6G	AL684370 Penicilli
c	42	15.4	85.6	988	8	AK061421	AK061421 Oryza sat
c	43	15.4	85.6	1028	8	AK104181	AK104181 Oryza sat
c	44	15.4	85.6	1032	8	AK061195	AK061195 Oryza sat
c	45	15.4	85.6	1039	8	AK104630	AK104630 Oryza sat

ALIGNMENTS

RESULT 1
SHE581560/c
LOCUS SHE581560 1405 bp DNA linear VRL 27-APR-2004
DEFINITION Suid herpesvirus 1 strain Kaplan partial ORF1.2 and left end of unique long region.
ACCESSION AJ581560
VERSION AJ581560.1 GI:34368527
KEYWORDS ORF1.2; unique long region.
SOURCE Suid herpesvirus 1 strain Kaplan
ORGANISM Suid herpesvirus 1 strain Kaplan
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1
AUTHORS Klupp,B.G., Hengartner,C.J., Mettenleiter,T.C. and Enquist,L.W.
TITLE Complete, annotated sequence of the pseudorabies virus genome
JOURNAL J. Virol. 78 (1), 424-440 (2004)
PUBMED 14671123
REFERENCE 2 (bases 1 to 1405)
AUTHORS Klupp,B.G.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) Klupp B.G., Institute of Molecular Biology, FedResCen Virus Diseases of Animals, Boddenblick 5A, D-17493 Greifswald - Insel Riems, GERMANY
FEATURES Location/Qualifiers
source 1. .1405
/organism="Suid herpesvirus 1 strain Kaplan"
/virion
/mol_type="genomic DNA"
/strain="Kaplan"
/db_xref="taxon:33703"
repeat_unit 3. .84
/note="inverted repeat of 442. .523"
/rpt_type=INVERTED
repeat_region 156. .251
/note="spaced direct imperfect repeats"
/rpt_type=DIRECT
/rpt_unit="156. .183"
repeat_unit complement(442. .523)
/note="inverted repeat of 3. .84"
/rpt_type=INVERTED
repeat_region 529. .655
/note="3 spaced imperfect repeats"

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                     /rpt_type=DIRECT
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     repeat_region   751. .958
                     /rpt_type=DIRECT
                     /rpt_unit="751. .776"
     CDS             1252. .>1405
                     /note="ORF1.2"
                     /codon_start=1
                     /product="ORF1.2 protein"
                     /protein_id="CAE46334.1"
                     /db_xref="GI:34368528"
                     /translation="MGGGTRGSDAPTWCHTRPTPRSFSRAARPDPAEPDVGRETGMDV
                     ERGTAAG"
     CDS             1375. .>1405
                     /note="ORF1.2
                     alternative"
                     /codon_start=1
                     /product="ORF1.2 protein"
                     /protein_id="CAE46335.1"
                     /db_xref="GI:34368529"
                     /translation="MDVERGTAAG"
ORIGIN

  Query Match             94.4%;  Score 17;  DB 14;  Length 1405;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGG 17
              |||||||||||||||||
Db       1168 TGCGCCGGCGCAGGGGG 1152


RESULT 2
AC144804/c
LOCUS       AC144804               232176 bp    DNA     linear   HTG 24-JUN-2003
DEFINITION  Gallus gallus clone CH261-22A23, WORKING DRAFT SEQUENCE, 14 ordered
            pieces.
ACCESSION   AC144804
VERSION     AC144804.1  GI:30962733
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 232176)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 232176)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
REFERENCE   3  (bases 1 to 232176)
  AUTHORS   Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
            Peng,Z., Malinov,I. and Rubin,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2003) Genome Sciences, Lawrence Berkeley National
            Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT
            Sequence Produced by Berkeley PGA
            Web site: http://pga.lbl.gov
            Center Code: PGABERK
            Center Project Name: G104
            Bac Clone Name: CH261-22A23

            This sequence has been compared to sequences of other species
            using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
            viewed at:
            http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=SREBF1

            The order-orientation of the draft sequence was accomplished by
            using:
            Avid (http://baboon.math.berkeley.edu/mavid),
            Lagan (http://lagan.stanford.edu/) and paired end information.

            Funding agent: Programs for Genomic Applications (NHLBI)

            Summary Statistics:
            Sequencing vector: Plasmid; pUC18
            Chemistry: Dye-terminator Big Dye
            Assembly program: Phrap version 0.990329.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 14 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1     1187: contig of 1187 bp in length
            *     1188     1287: gap of unknown length
            *     1288    12634: contig of 11347 bp in length
            *    12635    12734: gap of unknown length
            *    12735    16456: contig of 3722 bp in length
            *    16457    16556: gap of unknown length
            *    16557    26480: contig of 9924 bp in length
            *    26481    26580: gap of unknown length
            *    26581    29898: contig of 3318 bp in length
            *    29899    29998: gap of unknown length
            *    29999    36595: contig of 6597 bp in length
            *    36596    36695: gap of unknown length
            *    36696    39486: contig of 2791 bp in length
            *    39487    39586: gap of unknown length
            *    39587    42321: contig of 2735 bp in length
            *    42322    42421: gap of unknown length
            *    42422   116738: contig of 74317 bp in length
            *   116739   116838: gap of unknown length
            *   116839   159322: contig of 42484 bp in length
            *   159323   159422: gap of unknown length
            *   159423   177789: contig of 18367 bp in length
            *   177790   177889: gap of unknown length
            *   177890   181431: contig of 3542 bp in length
            *   181432   181531: gap of unknown length
            *   181532   229280: contig of 47749 bp in length
            *   229281   229380: gap of unknown length
            *   229381   232176: contig of 2796 bp in length.
FEATURES             Location/Qualifiers
     source          1. .232176
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9031"
                     /clone="CH261-22A23"
ORIGIN

  Query Match             94.4%;  Score 17;  DB 2;  Length 232176;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGG 17
              |||||||||||||||||
Db     177704 TGCGCCGGCGCAGGGGG 177688


RESULT 3
AR496235/c
LOCUS       AR496235                 448 bp    DNA     linear   PAT 22-SEP-2004
DEFINITION  Sequence 1195 from patent US 6703491.
ACCESSION   AR496235
VERSION     AR496235.1  GI:52431710
KEYWORDS    .
SOURCE      Unknown.
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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 448)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L., Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 1195 09-MAR-2004;
FEATURES Location/Qualifiers
source 1. .448
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 448;
Best Local Similarity 94.4%; Pred. No. 9.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||| |||||||
Db 20 TGCGCCGGCGGAGGGGGG 3

RESULT 4
AR511517/c
LOCUS AR511517 448 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 16477 from patent US 6703491.
ACCESSION AR511517
VERSION AR511517.1 GI:52446992
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 448)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L., Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 16477 09-MAR-2004;
FEATURES Location/Qualifiers
source 1. .448
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 448;
Best Local Similarity 94.4%; Pred. No. 9.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||| |||||||
Db 20 TGCGCCGGCGGAGGGGGG 3

RESULT 5
AK122136/c
LOCUS AK122136 616 bp mRNA linear PLN 29-OCT-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J033135J16, full insert sequence.
ACCESSION AK122136
VERSION AK122136.1 GI:37991782
KEYWORDS FLI_CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764
REFERENCE 2
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakahama,Y., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
TITLE Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 616)
AUTHORS Kikuchi,S.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT This clone is one of the 32K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,

Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.

FEATURES Location/Qualifiers
source 1. .616
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033135J16"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 616;
Best Local Similarity 94.4%; Pred. No. 8.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||||||||||| |
Db 224 TGCGCCGGCGCAGGGGAG 207

RESULT 6
AK060251/c
LOCUS AK060251 1665 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:001-004-C03, full insert sequence.
ACCESSION AK060251
VERSION AK060251.1 GI:32970269
KEYWORDS FLI_CDNA; oligo-capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764
REFERENCE 2 (bases 1 to 1665)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES Location/Qualifiers
source 1. .1665
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-004-C03"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 1665;
Best Local Similarity 94.4%; Pred. No. 7.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||||||||||| |
Db 1338 TGCGCCGGCGCAGGGGAG 1321

RESULT 7
AB017578S1
LOCUS AB017578S1 4225 bp DNA linear ROD 20-NOV-1999
DEFINITION Rattus norvegicus gene for cGMP-binding cGMP-specific phosphodiesterase, exon1a, exon1b and 5'-flanking region.
ACCESSION AB017578
VERSION AB017578.1 GI:5926761
KEYWORDS cGMP-binding cGMP-specific phosphodiesterase; alternative splicing.
SEGMENT 1 of 3
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```
REFERENCE   1
  AUTHORS   Kotera,J., Fujishige,K., Imai,Y., Kawai,E., Michibata,H.,
            Akatsuka,H., Yanaka,N. and Omori,K.
  TITLE     Genomic origin and transcriptional regulation of two variants of
            cGMP-binding cGMP-specific phosphodiesterases
  JOURNAL   Eur. J. Biochem. 262 (3), 866-873 (1999)
  MEDLINE   99339957
   PUBMED   10411650
REFERENCE   2  (bases 1 to 4225)
  AUTHORS   Omori,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-1998) Kenji Omori, Tanabe Seiyaku Co. Ltd.,
            Discovery Research Laboratory, Basic Technology Department; 2-50
            Kawagishi-2-chome, Toda, Saitama 335-8505, Japan
            (E-mail:k-omori@tanabe.co.jp, Tel:+81-48-433-8069,
            Fax:+81-48-433-8159)
FEATURES             Location/Qualifiers
     source          1. .4225
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                     /mol_type="genomic DNA"
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     exon            2765. .2886
                     /product="cGMP-binding cGMP-specific phosphodiesterase"
                     /note="alternative splicing
                     exon1a"
     exon            3244. .4166
                     /product="cGMP-binding cGMP-specific phosphodiesterase"
                     /note="alternative splicing
                     exon1b"
ORIGIN

  Query Match            91.1%;  Score 16.4;  DB 10;  Length 4225;
  Best Local Similarity  94.4%;  Pred. No. 5.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||| ||||||||||
Db       3447 TGCGCCGCCGCAGGGGGG 3464


RESULT 8
AY422718/c
LOCUS       AY422718                4898 bp    DNA     linear   BCT 26-OCT-2003
DEFINITION  Pseudomonas sp. K82 catechol 2,3 gene cluster, partial sequence.
ACCESSION   AY422718
VERSION     AY422718.1  GI:37790591
KEYWORDS    .
SOURCE      Pseudomonas sp. K82
  ORGANISM  Pseudomonas sp. K82
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Pseudomonadaceae; Pseudomonas.
REFERENCE   1  (bases 1 to 4898)
  AUTHORS   Kim,S.-I., Kim,J.-Y. and Kim,E.-A.
  TITLE     Proteome analysis of aromatic compounds degrading bacterium,
            Pseudomonas sp. K82
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4898)
  AUTHORS   Kim,S.-I.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-SEP-2003) Proteome Analysis, Korea Basic Science
            Institute, 52, Yeoeun-Dong, Yusung-Ku, Daejon 305-806, Korea
FEATURES             Location/Qualifiers
     source          1. .4898
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                     /strain="K82"
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                     /db_xref="GI:37790593"
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                     AVPVQGDEHWRCYSITSAPEDGQAISVLVRRVAGGRVSNWLCDHARAGQRLQVLPPAG
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                     GIEPSRVYREDFGAALEGAVETGAEGPDAELTVQLKGQTHTVSVRGGQFLLGAMLDAR
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                     KIGAVAVGAYASRAYLARHDTSASNPAFVDDHDLLAMNLQFFHQDHNFTYANLDWAKF
                     GLTGKVRVQSDSFVPMAHLCALGHGVALLPKFVAADYPELVPYPEKLPFETELWLVSR
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                     RMLQFKLPSGHEMRLYASKEFVGTDVGNINPDPWPDGLKGAGAHWLDHCLLMCEMNPE
                     AGINTVADNTRFMTEALDFFLTEQVLVGPEGNMQAATWMARTTTPHDIAFVGGPRSGL
                     HHIAFFLDSWHDVLKSADVMAKTKTRIDVAPTRHGITRGETIYFFDPSGNRNETFAGL
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                     /db_xref="GI:37790597"
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                     /db_xref="GI:37790598"
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                     WKVGPALACRQHQSSVKPSEETPATATLLGEVMNAVGVPKGSVPGAARLRPRLGRRI"
ORIGIN

  Query Match            91.1%;  Score 16.4;  DB 1;  Length 4898;
  Best Local Similarity  94.4%;  Pred. No. 5.8e+03;
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  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db       1519 TGCGCCGGCGCAGGGTGG 1502


RESULT 9
AB004065/c
LOCUS       AB004065               5278 bp    DNA     linear   BCT 27-FEB-2002
DEFINITION  Pseudomonas sp. genes for ORF1, ORF2, ORF3, chloroplast-type
            ferredoxin, catechol 2,3-dioxygenase, 2-hydroxymuconic
            6-semialdehyde dehydrogenase, partial and complete cds.
ACCESSION   AB004065 D86528
VERSION     AB004065.1  GI:11610562
KEYWORDS    2-hydroxymuconic 6-semialdehyde dehydrogenase; catechol
            2,3-dioxygenase; chloroplast-type ferredoxin; ORF3; ORF2; ORF1.
SOURCE      Pseudomonas sp.
  ORGANISM  Pseudomonas sp.
            Bacteria; Proteobacteria.
REFERENCE   1
  AUTHORS   Murakami,S., Nakanishi,Y., Kodama,N., Takenaka,S., Shinke,R. and
            Aoki,K.
  TITLE     Purification, characterization, and gene analysis of catechol
            2,3-dioxygenase from the aniline-assimilating bacterium Pseudomonas
            species AW-2
  JOURNAL   Biosci. Biotechnol. Biochem. 62 (4), 747-752 (1998)
  MEDLINE   98276889
   PUBMED   9614705
REFERENCE   2  (bases 1 to 5278)
  AUTHORS   Murakami,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-1997) Shuichiro Murakami, Kobe University,
            Department of Biofunctional Chemistry; 1-1 Rokkodai-cho, Nada-ku,
            Kobe 657, Japan (E-mail:hakko2@kobe-u.ac.jp, Tel:81-78-803-0681,
            Fax:81-78-803-0680)
COMMENT     D86528:Submitted (08-Jul-1996).
FEATURES             Location/Qualifiers
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                     LQAGSGQRLEIRHWYDAEQGLPTQALLEAQTQGLEAADAYLCGPEAFMHSVLAALAAA
                     GIEPSRVYREDFGAALEGAVETGAEGPDAELTVQLKGQTHTVSVRGGQFLLGAMLDAG
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                     RVLEQRFGRTLFVRSEAGWKASADLHALVSAAQHMEEAARSFSQNHQEGAGVVRISLM
                     DVFAKRFAPVFVALGEKFPRLLLNITTETHFVNLEQDQVDIAVRLARPVRNSNSLRVR
                     KIGAVAVGAYASRAYLARHDTSASNPAFVDDHDLLAMNLQFFHQDHNFTYANLDWAKF
                     GLTGKVRVQSDSFVPMAHLCALGHGVALLPKFVAADYPELVPYPEKLFFETELWLVSR
                     FDLLAAWQRELADRLQEEMATWPQ"
     gene            2403. .2678
                     /gene="alnD"
     CDS             2403. .2678
                     /gene="alnD"
                     /function="electron transfer protein"
                     /codon_start=1
                     /evidence=not_experimental
                     /transl_table=11
                     /product="chloroplast-type ferredoxin"
                     /protein_id="BAB18932.1"
                     /db_xref="GI:11610566"
                     /translation="MVRLGRKGIPVGCVNGGCGVCKVRIVEGQIKALGPISRAHVTLD
                     EENQGYTLACRVAPQTPVNLEVAGKLSKPFSKGRAESATASPSIQQQ"
     gene            2700. .3644
                     /gene="alnE"
     CDS             2700. .3644
                     /gene="alnE"
                     /EC_number="1.13.11.2"
                     /function="meta-cleavage of catechol"
                     /codon_start=1
                     /evidence=experimental
                     /transl_table=11
                     /product="catechol 2,3-dioxygenase"
                     /protein_id="BAB18933.1"
                     /db_xref="GI:11610567"
                     /translation="MGVMRIGHASLKVMDMDAAVRHYENVLGMKTTMKDKAGNVYLKC
                     WDEWDKYSVILTPSDQAGMNHLAYKVEKEADLEALQQKIEAWGVKTTMLDEGTLPSTG
                     RMLQFKLPSGHEMRLYASKEFVGTDVGNINPDPWPDGLKGAGAHWLDHCLLMCEMNPE
                     AGINTVADNTRFMTEALDFFLTEQVLVGPEGNMQAATWMARTTTPHDIAFVGGPRSGL
                     HHIAFFLDSWHDVLKSADVMAKTKTRIDVAPTRHGITRGETIYFFDPSGNRNETFAGL
                     GYLAQRDRPVTTWTEDQLGSGIFYHTGYLVPSFTEVYT"
     gene            4245. .4808
                     /gene="alnG"
     CDS             4245. .4808
                     /gene="alnG"
                     /note="7 amino acids coded by Tn5 attached at C terminal."
                     /codon_start=1
                     /evidence=experimental
                     /transl_table=11
                     /product="2-hydroxymuconic 6-semialdehyde dehydrogenase"
                     /protein_id="BAB18934.1"
                     /db_xref="GI:11610568"
                     /translation="MKQFLNFINGDFVATAKTFENRNPATNEVVGLVHEAGQAEVDAA
                     VAAGRAALKGEWGTMSVVKRAELLHAVADEINRRFDDFLAAELADTGKPRSLASHIDI
                     PRGAANFKIFADIVKNVPTESFQMTTPDGGTAISYGLRTPLGVVGVICPWNLPLLLMT
                     WKVGPALACGNTVIVKPSEETLTLIHK"
     misc_recomb     4788. .5278
                     /note="transposon Tn5-Mob"
                     /organism="Escherichia coli"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 1;  Length 5278;
  Best Local Similarity   94.4%;  Pred. No. 5.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||||||||||| ||
Db       1519 TGCGCCGGCGCAGGGTGG 1502


RESULT 10
AC151612
LOCUS       AC151612               34503 bp    DNA     linear   HTG 21-SEP-2004
DEFINITION  Emiliania huxleyi clone JGIACCU-13I1, WORKING DRAFT SEQUENCE, 3
            unordered pieces.
```

```
ACCESSION   AC151612
VERSION     AC151612.1  GI:52353786
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Emiliania huxleyi
  ORGANISM  Emiliania huxleyi
            Eukaryota; Haptophyceae; Isochrysidales; Emiliania.
REFERENCE   1  (bases 1 to 34503)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Unpublished
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 34503)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-SEP-2004) Production Genomics Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
            94598-1698, USA
COMMENT     -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -------
            Project Information
            Center Project Name: 3633987
            Center clone name: JGI-ACCU_13I1
            -------
            Summary Statistics
            Consensus quality: 34155 bases at least Q40
            Consensus quality: 34270 bases at least Q30
            Consensus quality: 34288 bases at least Q20
            Estimated insert size: 40000; agarose-fp estimation
            Estimated insert size: 34303; sum-of-contigs estimation
            Quality coverage:  18.2 in Q20 bases; agarose-fp estimation
            Quality coverage:  21.22 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2928: contig of 2928 bp in length
            *     2929     3028: gap of unknown length
            *     3029     6325: contig of 3297 bp in length
            *     6326     6425: gap of unknown length
            *     6426    34503: contig of 28078 bp in length.
FEATURES             Location/Qualifiers
     source          1. .34503
                     /organism="Emiliania huxleyi"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:2903"
                     /clone="JGIACCU-13I1"
                     /clone_lib="JGI Fosmid library ACCU"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 2;  Length 34503;
  Best Local Similarity   94.4%;  Pred. No. 3.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||||||||||| |||
Db       6682 TGCGCCGGCGCAGGCGGG 6699


RESULT 11
CQ861719
LOCUS       CQ861719               96256 bp    DNA     linear   PAT 10-SEP-2004
DEFINITION  Sequence 352 from Patent WO2004072265.
ACCESSION   CQ861719
VERSION     CQ861719.1  GI:51982708
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burczynski,M., Twine,N., Dorner,A.J. and Trepicchio,W.L.
  TITLE     METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i
  JOURNAL   Patent: WO 2004072265-A 352 26-AUG-2004;
            Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
            Dorner, Andrew J. (US); Trepicchio, William L. (US)
FEATURES             Location/Qualifiers
     source          1. .96256
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 96256;
  Best Local Similarity   94.4%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              | ||||||||||||||||
Db      21755 TCCGCCGGCGCAGGGGGG 21772


RESULT 12
HS1177I5
LOCUS       HS1177I5               96256 bp    DNA     linear   PRI 05-JUN-2003
DEFINITION  Human DNA sequence from clone RP5-1177I5 on chromosome 22q13.1
            Contains a novel gene, the MSE55 gene for serum constituent protein
            MSE55, the LGALS2 gene for soluble Galactose-binding Lectin 2
            (Galectin 2, S-Lac Lectin 2, HL14), ESTs, an STS, GSSs and two
            putative CpG islands, complete sequence.
ACCESSION   AL022315
VERSION     AL022315.1  GI:3820991
KEYWORDS    HTG; CpG island; galectin; lectin; LGALS2; MSE55.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 96256)
  AUTHORS   Coville,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 2, 1998 this sequence version replaced gi:3550020.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep ----------
            Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            This sequence was generated from part of bacterial clone contigs of
            human chromosome 22, constructed by the Sanger Centre Chromosome 22
```

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          Mapping Group.  Further information can be found at
          http://www.sanger.ac.uk/HGP/Chr22
          RP5-1177I5 is from the library RPCI-5 constructed by the group of
          Pieter de Jong. For further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2
          This sequence is the entire insert of clone RP5-1177I5.
FEATURES             Location/Qualifiers
     source          1. .96256
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="22"
                     /map="q13.1"
                     /clone="RP5-1177I5"
                     /clone_lib="RPCI-5"
     repeat_region   1. .231
                     /note="AluSq repeat: matches 59..299 of consensus"
     repeat_region   complement(480. .554)
                     /note="MIR repeat: matches 186. .262 of consensus"
     repeat_region   1092. .1102
                     /note="2.2 copies 5 mer CCTGG 22% conserved"
     repeat_region   1260. .1278
                     /note="19.0 copies 1 mer G 29% conserved"
     repeat_region   1666. .1775
                     /note="MIR repeat: matches 29. .137 of consensus"
     repeat_region   1851. .1877
                     /note="3.0 copies 9 mer CCACCCACC 36% conserved"
     repeat_region   1863. .1874
                     /note="2.4 copies 5 mer CCCAC 24% conserved"
     repeat_region   1967. .2076
                     /note="L2 repeat: matches 2986. .3098 of consensus"
     repeat_region   2294. .2310
                     /note="2.4 copies 7 mer AGCTACC 25% conserved"
     repeat_region   2321. .2334
                     /note="2.8 copies 5 mer GTCAG 28% conserved"
     repeat_region   2358. .2379
                     /note="2.4 copies 9 mer TCTGCCAGC 44% conserved"
     repeat_region   complement(2493. .2617)
                     /note="MIR repeat: matches 60. .212 of consensus"
     repeat_region   2735. .2755
                     /note="2.1 copies 10 mer CTCCAGTGCT 35% conserved"
     repeat_region   2853. .2868
                     /note="2.3 copies 7 mer CCACCAT 23% conserved"
     repeat_region   2900. .2911
                     /note="2.4 copies 5 mer AGGGC 24% conserved"
     repeat_region   3071. .3174
                     /note="MIR repeat: matches 84. .191 of consensus"
     repeat_region   complement(3188. .3399)
                     /note="MIR repeat: matches 36. .262 of consensus"
     repeat_region   3462. .3483
                     /note="3.7 copies 6 mer TCTCCC 37% conserved"
     repeat_region   3466. .3483
                     /note="3.6 copies 5 mer CCTCT 27% conserved"
     repeat_region   3494. .3523
                     /note="15.0 copies 2 mer CT 51% conserved"
     repeat_region   3719. .3736
                     /note="2.2 copies 8 mer GGAGGAAG 36% conserved"
     repeat_region   4020. .4132
                     /note="MIR repeat: matches 60. .169 of consensus"
     repeat_region   4270. .4284
                     /note="5.0 copies 3 mer CCT 21% conserved"
     repeat_region   complement(4630. .4853)
                     /note="MIR repeat: matches 16. .253 of consensus"
     repeat_region   5577. .5604
                     /note="2.5 copies 11 mer GGGCAGAGAGA 38% conserved"
     repeat_region   5817. .5876
                     /note="L2 repeat: matches 3003. .3060 of consensus"
     repeat_region   5878. .5895
                     /note="3.0 copies 6 mer CCCTCA 29% conserved"
     repeat_region   5879. .5895
                     /note="3.4 copies 5 mer CCTCA 25% conserved"
     repeat_region   6852. .6914
                     /note="MIR repeat: matches 81. .143 of consensus"
     repeat_region   7058. .7069
                     /note="2.4 copies 5 mer GAGGG 24% conserved"
     repeat_region   7140. .7157
                     /note="3.6 copies 5 mer GGAGA 29% conserved"
     repeat_region   complement(7185. .7506)
                     /note="L2 repeat: matches 2917. .3259 of consensus"
     repeat_region   7637. .7650
                     /note="14.0 copies 1 mer A 28% conserved"
     repeat_region   7755. .8018
                     /note="AluSx repeat: matches 1. .302 of consensus"
     repeat_region   8067. .8176
                     /note="MIR3 repeat: matches 49. .171 of consensus"
     repeat_region   8242. .8260
                     /note="2.4 copies 8 mer GCACACAG 29% conserved"
     repeat_region   8365. .8386
                     /note="4.4 copies 5 mer CCAGC 26% conserved"
     repeat_region   8754. .8765
                     /note="2.4 copies 5 mer GGGGA 24% conserved"
     repeat_region   complement(8836. .9040)
                     /note="MIR repeat: matches 13. .262 of consensus"
     repeat_region   9235. .9333
                     /note="MER5A repeat: matches 63. .163 of consensus"
     repeat_region   9358. .9652
                     /note="AluSx repeat: matches 1. .303 of consensus"
     gene            complement(join(10190. .10315,10888. .10998))
                     /gene="dJ1177I5.1"
     CDS             complement(join(<10190. .10315,10888. .>10998))
                     /gene="dJ1177I5.1"
                     /note="supported by predicted exons
                     match: ESTs: Em:AA316883"
                     /codon_start=1
                     /evidence=not_experimental
                     /product="dJ1177I5.1 (PUTATIVE novel protein)"
                     /protein_id="CAB42832.1"
                     /db_xref="GI:4808220"
                     /translation="DILEHDWREAQDSRQELCQKLHAVQGELQWAEELRDQYLQEMED
                     LRLKHRTLQKDCDLYKHRMATVLAQLEEIEKERDQ"
     repeat_region   10413. .10522
                     /note="MIR repeat: matches 43. .153 of consensus"
     repeat_region   10579. .10750
                     /note="L2 repeat: matches 3103. .3269 of consensus"
     repeat_region   10863. .10882
                     /note="4.0 copies 5 mer GGGCA 31% conserved"
     repeat_region   11054. .11064
                     /note="2.2 copies 5 mer CAGGG 22% conserved"
     repeat_region   11102. .11111
                     /note="2.5 copies 4 mer GGAA 20% conserved"
     repeat_region   11139. .11275
                     /note="MIR repeat: matches 70. .198 of consensus"
     repeat_region   11485. .11499
                     /note="2.5 copies 6 mer CCCACA 21% conserved"
     repeat_region   11591. .11611
                     /note="1.9 copies 11 mer CTGACCTGCCA 42% conserved"
     repeat_region   11934. .11947
                     /note="2.3 copies 6 mer ACCCCC 28% conserved"
     repeat_region   11967. .12590
                     /note="15.6 copies 40 mer
                     GCCCTGGTACCTGCTGCAGGCCCTCCTGACCACCCCCCAG 526% conserved"
     repeat_region   12128. .12139
                     /note="2.0 copies 6 mer CCCATG 24% conserved"
     repeat_region   12441. .12452
                     /note="2.0 copies 6 mer GCCCTG 24% conserved"
     repeat_region   12557. .12569
                     /note="2.2 copies 6 mer GCCCTG 26% conserved"
     repeat_region   12663. .12697
                     /note="5.8 copies 6 mer CTCCTT 70% conserved"
     repeat_region   12763. .12775
                     /note="2.2 copies 6 mer TTGAGC 26% conserved"
     repeat_region   13154. .13468
                     /note="AluSx repeat: matches 1. .308 of consensus"
     repeat_region   13480. .13747
                     /note="AluJb repeat: matches 30. .311 of consensus"
```

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     repeat_region   13760. .13846
                     /note="29.0 copies 3 mer GAG 77% conserved"
     repeat_region   13762. .13784
                     /note="2.1 copies 11 mer GGAGGAGGAGG 46% conserved"
     repeat_region   13779. .13788
                     /note="2.5 copies 4 mer GGAG 20% conserved"
     repeat_region   13860. .13880

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 96256;
  Best Local Similarity   94.4%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              | ||||||||||||||||
Db      21755 TCCGCCGGCGCAGGGGGG 21772


RESULT 13
AC149892
LOCUS       AC149892               98359 bp    DNA     linear   HTG 24-JUN-2004
DEFINITION  Xenopus tropicalis clone ISB-242D2, WORKING DRAFT SEQUENCE, 8
            unordered pieces.
ACCESSION   AC149892
VERSION     AC149892.1  GI:49170149
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Xenopus tropicalis (Silurana tropicalis)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 98359)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Unpublished
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 98359)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2004) Production Genomics Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
            94598-1698, USA
COMMENT     -------Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -------
            Project Information
            Center Project Name: 2865953
            Center clone name: ISB-242D2
            -------
            Summary Statistics
            Consensus quality: 95112 bases at least Q40
            Consensus quality: 96157 bases at least Q30
            Consensus quality: 96888 bases at least Q20
            Estimated insert size: 104000; agarose-fp estimation
            Estimated insert size: 97659; sum-of-contigs estimation
            Quality coverage:  15.53 in Q20 bases; agarose-fp estimation
            Quality coverage:  16.54 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2277: contig of 2277 bp in length
            *     2278     2377: gap of unknown length
            *     2378     5120: contig of 2743 bp in length
            *     5121     5220: gap of unknown length
            *     5221     8464: contig of 3244 bp in length
            *     8465     8564: gap of unknown length
            *     8565    19956: contig of 11392 bp in length
            *    19957    20056: gap of unknown length
            *    20057    30478: contig of 10422 bp in length
            *    30479    30578: gap of unknown length
            *    30579    41700: contig of 11122 bp in length
            *    41701    41800: gap of unknown length
            *    41801    52925: contig of 11125 bp in length
            *    52926    53025: gap of unknown length
            *    53026    98359: contig of 45334 bp in length.
FEATURES             Location/Qualifiers
     source          1. .98359
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:8364"
                     /clone="ISB-242D2"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 2;  Length 98359;
  Best Local Similarity   94.4%;  Pred. No. 3.2e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||||| |||||||||
Db      32227 TGCGCCGGGGCAGGGGGG 32244


RESULT 14
AC103564
LOCUS       AC103564               106117 bp    DNA     linear   PRI 23-MAR-2002
DEFINITION  Homo sapiens BAC clone RP11-788A1 from 2, complete sequence.
ACCESSION   AC103564
VERSION     AC103564.5  GI:19482407
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 106117)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 106117)
  AUTHORS   VanBrunt,A., Kozlowicz,A. and Spalding,L.
  TITLE     The sequence of Homo sapiens BAC clone RP11-788A1
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 106117)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-NOV-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 106117)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 106117)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 106117)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Mar 15, 2002 this sequence version replaced gi:18677687.
            ------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
```

```
            Contact: sapiens@watson.wustl.edu
          -------------- Summary Statistics
            Center project name: H_NH0788A01
          --------------.

          NOTICE:  This sequence may not represent the entire insert of this
          clone.  It may be shorter because we only sequence overlapping
          clone sections once, or longer because we provide a small overlap
          between neighboring data submissions.

          This sequence was finished as follows unless otherwise noted:
          all regions were double stranded, sequenced with an alternate
          chemistry, or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by sequence
          from more than one subclone; and the assembly was confirmed by
          restriction digest.

          MAPPING INFORMATION:
          Mapping information for this clone was provided by Dr. John D.
          McPherson, Department of Genetics, Washington University, St. Louis
          MO. For additional information about the map position of this
          sequence, see http://genome.wustl.edu/gsc

          SOURCE INFORMATION:
          The RPCI-11 human BAC library was made from the blood of one male
          donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
          Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
          approach for construction of bacterial artificial chromosome
          libraries. Genomics 51:1-8. The clone may be obtained either from
          Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
          and coworkers at http://www.chori.org
          VECTOR:  pBACe3.6

          NEIGHBORING SEQUENCE INFORMATION:
          The clone sequenced to the right is AJ239322, 2000 bp overlap.
          Actual start of this clone is at base position 1 of RP11-788A1.

          Polymorphisms exist between AC103564, AC093724 and AJ239322. Data
          from AC093724 was used to finish AC103564.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="2"
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     repeat_region   1743. .2012
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     repeat_region   2213. .2320
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     repeat_region   2451. .2767
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     repeat_region   2772. .2914
                     /rpt_family="L1"
     repeat_region   2915. .3208
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     repeat_region   3209. .3921
                     /rpt_family="L1"
     repeat_region   4396. .5149
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     repeat_region   5153. .5365
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     repeat_region   5421. .5535
                     /rpt_family="ERV1"
     repeat_region   5536. .5999
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     misc_feature    5977. .6763
                     /note="match to EST BG221914 (NID:g13747935)"
     misc_feature    6031. .6813
                     /note="match to EST BG221911 (NID:g13747932)"
     repeat_region   6245. .6660
                     /rpt_family="MaLR"
     repeat_region   6661. .7534
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     repeat_region   7537. .8028
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     repeat_region   8037. .8331
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     repeat_region   8359. .8990
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     repeat_region   8993. .9386
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     misc_feature    10006. .10226
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     misc_feature    10259. .10262
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  Best Local Similarity   94.4%;  Pred. No. 3.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||||||| ||||||
Db      24281 TGCGCCGGCGCTGGGGGG 24298


RESULT 15
AP005064/c
LOCUS       AP005064              155303 bp    DNA     linear   PLN 28-JUL-2004
DEFINITION  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
            BAC clone:OSJNBa0049G15.
ACCESSION   AP005064
VERSION     AP005064.3  GI:40253534
KEYWORDS    .
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Katayose,Y.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
            clone:OSJNBa0049G15
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 155303)
  AUTHORS   Sasaki,T., Matsumoto,T. and Katayose,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-APR-2002) Takuji Sasaki, National Institute of
            Agrobiological Sciences, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     On Dec 19, 2003 this sequence version replaced gi:30984143.
            Genes were predicted from the integrated results of the following:
            GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
            (http://www.softberry.com/), GeneMark.hmm
            (http://opal.biology.gatech.edu/GeneMark/), GlimmerM
            (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM
            (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
            (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
            (http://globin.cse.psu.edu/html/docs/sim4.html), gap2
            (http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The
            genomic sequence was searched against NCBI NonRedundant Protein
            database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
            sequence database at RGP or DDBJ. Protein homologies of the coding
            regions were searched against NCBI NonRedundant Protein database
            with BLASTP. ESTs represent the identified cDNA sequences using
            BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
            Full-length cDNAs represent the identified cDNA sequences using
            BLASTN with the corresponding DDBJ accession no.
            A gene with identity or significant homology to a protein is
            classified based on the protein name to indicate the homology level
            such as same name, 'putative-' and '-like protein'. A gene without
            significant homology to any protein but with full-length cDNA or
            EST homology (covering almost the entire length of partial
            sequence) is classified as an 'unknown' protein. A gene predicted
            by two or more gene prediction programs is classified as a
            'hypothetical' protein according to IRGSP standard. A gene
            predicted by a single gene prediction program is also classified as
            a probable 'hypothetical' protein and is included as a
            miscellaneous feature of the sequence.
            The orientation of the sequence is from -21M13 to M13rev of the BAC
            clone. This sequence of OSJNBa0049G15 clone has an overlap with
            OJ1033_B09 (DDBJ: AP003859) clone at 5' end and with OSJNBb0003H03
            (DDBJ: AP005495) clone at 3' end. Detailed information on overlap
            and assembly quality together with annotation of this entry is
            available at
            http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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                      this category is not included in IRGSP standard"
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                      ASWACEDSASLLKEIVRQLTSEEDGAQGSTSSTEQAGGAGAPNVRNLRQDVAAHLQSH
                      RYLIVIDDLKKVKVWSDIASAFPENNKGSRVIVTTSILSIATTCAYGSWVYKMQCLQK
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                DCCEEQLKVEKEVLQVISVWGTGSDLEMMSIKKAYDDTETMKSFNCRAWVKMVHPFHP
                IEFIRSLLAQFHKNVCPEQDNTVKILDLMVATDDVLIEEFKQQLSQKFLVVLEDVTTM
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                RQFFNNYMRQSSKNTVTRNPYYDKKKFGWVDVPRPRPFDLRDLSKSLHSELNPAFKDE
                VMSTIKDPIQQCREYLQREENWPYLIVIDGLQSKEEWDSIRRNMDFKFNTSSGKSNRS
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gene            50613. .54895
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  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db      65833 TGCGCCGGCGCAGGGGAG 65816


Search completed: April 29, 2005, 08:03:50
Job time : 716.341 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 183.527 Seconds
(without alignments)
580.598 Million cell updates/sec

Title: US-10-068-160A-17
Perfect score: 18
Sequence: 1 tgcgccggcgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	20	8	ACC48302	Acc48302 CpG oligo
	2	18	100.0	20	12	ADN96871	Adn96871 Immunosti
	3	16.4	91.1	96256	13	ADR53001	Adr53001 Drug ther
	4	16	88.9	963	11	ABD09335	Abd09335 Pseudomon
	5	16	88.9	1050	11	ABD09195	Abd09195 Pseudomon
c	6	15.4	85.6	374	4	AAL10608	Aal10608 Human bre
c	7	15.4	85.6	450	4	AAL17683	Aal17683 Human bre
c	8	15.4	85.6	499	3	AAC41286	Aac41286 Zea mays
c	9	15.4	85.6	513	11	ACN80806	Acn80806 Breast ca
c	10	15.4	85.6	564	12	ADL85306	Adl85306 DNA up-re
c	11	15.4	85.6	564	12	ADL85307	Adl85307 DNA up-re
c	12	15.4	85.6	597	12	ACH71251	Ach71251 Human gen
c	13	15.4	85.6	664	11	ACN86723	Acn86723 Breast ca
c	14	15.4	85.6	681	11	ADJ11795	Adj11795 Rice cDNA
c	15	15.4	85.6	684	11	ADJ11463	Adj11463 Rice DNA
c	16	15.4	85.6	745	11	ACN89965	Acn89965 Breast ca
	17	15.4	85.6	804	13	ADT43197	Adt43197 Bacterial
c	18	15.4	85.6	900	3	AAA79481	Aaa79481 Eucalyptu
c	19	15.4	85.6	969	8	ADA71180	Ada71180 Rice gene
c	20	15.4	85.6	1008	3	AAC56198	Aac56198 Eucalyptu
	21	15.4	85.6	1061	6	ABI99675	Abi99675 Mouse isc
	22	15.4	85.6	1250	10	ADE07415	Ade07415 Novel cod
	23	15.4	85.6	1404	8	ACA42729	Aca42729 Prokaryot
	24	15.4	85.6	1611	10	ADD49064	Add49064 Human NOV
c	25	15.4	85.6	1637	12	ADM47612	Adm47612 Polynucle
c	26	15.4	85.6	1842	13	ADS57886	Ads57886 Bacterial
	27	15.4	85.6	2071	6	ADH48763	Adh48763 NOV19 cod
c	28	15.4	85.6	2196	8	ADA69886	Ada69886 Rice gene
	29	15.4	85.6	2448	10	ADD29815	Add29815 Human tum
c	30	15.4	85.6	2478	3	AAA79707	Aaa79707 Eucalyptu
	31	15.4	85.6	2559	10	ADD15216	Add15216 Human ser
	32	15.4	85.6	2559	13	ADR25271	Adr25271 Breast ca
	33	15.4	85.6	2600	12	ADQ19921	Adq19921 Human sof
	34	15.4	85.6	2622	10	ADJ80233	Adj80233 Novel hum
c	35	15.4	85.6	2787	5	ABV21138	Abv21138 Human pro
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c	37	15.4	85.6	2929	5	ABV25833	Abv25833 Human pro
c	38	15.4	85.6	2929	5	ABV29359	Abv29359 Human pro
c	39	15.4	85.6	2929	5	ABV25524	Abv25524 Human pro
c	40	15.4	85.6	2929	5	ABV28091	Abv28091 Human pro
c	41	15.4	85.6	2929	5	ABV28883	Abv28883 Human pro
c	42	15.4	85.6	2929	5	ABV22253	Abv22253 Human pro
c	43	15.4	85.6	2929	5	ABV24150	Abv24150 Human pro
c	44	15.4	85.6	2929	5	ABV24860	Abv24860 Human pro
c	45	15.4	85.6	2929	5	ABV25159	Abv25159 Human pro

ALIGNMENTS

RESULT 1
ACC48302
ID ACC48302 standard; DNA; 20 BP.
XX
AC ACC48302;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide used for dendritic cell maturation.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1
FT /*tag= a
FT /note= "N is any base (especially G) or no base"
FT misc_difference 2
FT /*tag= b
FT /note= "N is any base (especially G) or no base"
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Disclosure; Page 26; 69pp; English.

XX
CC The present sequence is that of a D type CpG oligodeoxynucleotide that is
CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
CC invention. Mature dendritic cells are obtained by contacting a dendritic
CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
CC The method is useful for generating mature dendritic cells and enhancing
CC T cell responses, thus enhancing antigen presentation. Mature dendritic
CC cells are useful for tumour immunotherapy, for augmenting an immune
CC response to an infectious agent or to a vaccine, and as vaccines to
CC prevent future infection or to activate the immune system to treat
CC diseases such as cancer. Mature dendritic cells may also be used to
CC produce activated T lymphocytes
XX
SQ Sequence 20 BP; 1 A; 5 C; 11 G; 1 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGCCGGCGCAGGGGGG 20

RESULT 2
ADN96871
ID ADN96871 standard; DNA; 20 BP.
XX
AC ADN96871;
XX
DT 26-AUG-2004 (first entry)
XX
DE Immunostimulatory D CpG oligonucleotide seqid 5.
XX
KW virucide; anti-HIV; antibacterial; fungicide; cerebroprotective;
KW tuberculostatic; anti-inflammatory; hepatotropic; cytostatic;
KW dermatological; bacterial growth inhibitor; immunostimulator;
KW immune response; immunostimulatory; opportunistic infection;
KW lentivirus infection; human immunodeficiency virus infection; AIDS;
KW Leishmania infection; bacterial infection; fungal infection;
KW viral infection; protozoan infection; prion disease; nucleoplasm;
KW salmonellosis; syphilis; neurosyphilis; tuberculosis;
KW bacillary angiomatosis; aspergillosis; candidiasis; coccidioidomycosis;
KW cryptococcal meningitis; hepatitis B; histoplasmosis; cryptosporidiosis;
KW isosporiasis; microsporidiosis; pneumocystis carinii pneumonia;
KW toxoplasmosis; cytomegalovirus; hepatitis; herpes simplex; herpes zoster;
KW human papillomavirus; molluscum contagiosum; oral hairy leukoplakia;
KW progressive multifocal leukoencephalopathy; neoplasm; Kaposi's sarcoma;
KW systemic non-Hodgkin's lymphoma; primary central nervous system lymphoma;
KW HSV; genital herpes; HZV; shingles; genital wart; cervical cancer;
KW immunostimulatory CpG oligonucleotide; ss.
XX
OS Synthetic.
XX
PN US2004105872-A1.
XX
PD 03-JUN-2004.
XX
PF 17-SEP-2003; 2003US-00666022.
XX
PR 18-SEP-2002; 2002US-0411944P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Verthelyi D;
XX
DR WPI; 2004-419442/39.
XX
PT Increasing an immune response to an opportunistic infection e.g.
PT bacterial infections in an immunocompromised subject involves
PT administering immunostimulatory D oligodeoxynucleotide or an
PT immunostimulatory K oligodeoxynucleotide.
XX
PS Claim 21; SEQ ID NO 5; 64pp; English.
XX
CC The invention describes a method of increasing an immune response to an
CC opportunistic infection in an immunocompromised subject involves
CC administering an immunostimulatory D oligodeoxynucleotide or an
CC immunostimulatory K oligodeoxynucleotide, where an antigenic epitope of a
CC polypeptide is not administered to the subject. The method is useful for
CC increasing an immune response to an opportunistic infection e.g.
CC infection with a lentivirus such as human immunodeficiency virus
CC (including HIV-1, HIV-2) e.g. AIDS; infection with Leishmania; bacterial
CC infections; fungal infections; viral infections; protozoan infections;
CC prion disease; and nucleoplasm in an immunocompromised subject or a
CC subject infected with a lentivirus. The bacterial infections include
CC salmonellosis, syphilis and neurosyphilis, tuberculosis and bacillary
CC angiomatosis, the fungal infections include aspergillosis, candidiasis,
CC coccidioidomycosis, cryptococcal meningitis, hepatitis B, and
CC histoplasmosis, the protozoal infections include cryptosporidiosis,
CC isosporiasis, microsporidiosis, pneumocystis carinii pneumonia and
CC toxoplasmosis, viral infections include cytomegalovirus, hepatitis,
CC herpes simplex, herpes zoster, human papilloma virus, molluscum
CC contagiosum, oral hairy leukoplakia and progressive multifocal
CC leukoencephalopathy and neoplasms include Kaposi's sarcoma, systemic non-
CC Hodgkin's lymphoma and primary central nervous system lymphoma. The
CC herpes simplex includes HSV, genital herpes. The herpes zoster includes
CC HZV and shingles. The human papilloma virus includes HPV, genital warts
CC and cervical cancer. The method stimulates immune responses to any
CC opportunistic infection in immunocompromised subjects. This sequence
CC represents an immunostimulatory CpG oligonucleotide sequence that
CC stimulate the release of cytokines from cells of the immune system and
CC can be used to increase immune response in the method of the invention.
XX
SQ Sequence 20 BP; 1 A; 5 C; 11 G; 1 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||||||||||||
Db 3 TGCGCCGGCGCAGGGGGG 20

RESULT 3
ADR53001
ID ADR53001 standard; DNA; 96256 BP.
XX
AC ADR53001;
XX
DT 18-NOV-2004 (first entry)
XX
DE Drug therapy altered expressed gene #352.
XX
KW drug activity monitoring; expression profile; gene expression;
KW peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
KW CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
KW mTOR; ds.
XX
OS Homo sapiens.
XX
PN WO2004072265-A2.
XX
PD 26-AUG-2004.
XX
PF 11-FEB-2004; 2004WO-US004118.
XX
PR 11-FEB-2003; 2003US-0446133P.
PR 03-APR-2003; 2003US-0459782P.
PR 23-JAN-2004; 2004US-0538246P.
XX
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.

PA (TREP/) TREPICCHIO W L.
XX
PI Burczynski M, Twine N, Dorner AJ, Trepicchio WL;
XX
DR WPI; 2004-642301/62.
XX
PT Monitoring drug activities in vivo comprises comparing an expression
PT profile of a gene in a peripheral blood sample of a patient before and
PT after drug therapy.
XX
PS Disclosure; SEQ ID NO 352; 136pp; English.
XX
CC The invention relates to a method of monitoring drug activities in vivo
CC by comparing an expression profile of at least one gene in a peripheral
CC blood sample of a patient to a reference expression profile of the at
CC least one gene, where the at least one gene is differentially expressed
CC in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
CC blood disease and are subjected to a drug therapy as compared to PBMCs
CC isolated from the patient before the drug therapy, and where the patient
CC has the non-blood disease and is being treated by the drug therapy. The
CC method, kit, and nucleic acid array are useful for monitoring drug
CC activities in vivo. The drug is especially CCI-779, an ester analogue of
CC the immunosuppressant rapamycin which is a potent inhibitor of the
CC mammalian target of rapamycin (mTOR). This sequence represents a gene
CC expressed in PBMC altered by the drug therapy. (Note: this sequence does
CC no form part of the printed specification but was obtained in electronic
CC format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).
XX
SQ Sequence 96256 BP; 23707 A; 26405 C; 24812 G; 21332 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 13; Length 96256;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
| ||||||||||||||||
Db 21755 TCCGCCGGCGCAGGGGGG 21772

RESULT 4
ABD09335
ID ABD09335 standard; DNA; 963 BP.
XX
AC ABD09335;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7939.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75764.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7939; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 963 BP; 140 A; 330 C; 334 G; 159 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 11; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCCGGCGCAGGGGGG 18
||||||||||||||||
Db 906 CGCCGGCGCAGGGGGG 921

RESULT 5
ABD09195
ID ABD09195 standard; DNA; 1050 BP.
XX
AC ABD09195;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7799.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75624.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7799; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,

```
CC   for the ability to bind a P. aeruginosa nucleic acid, as components of
CC   effective antibacterial targets, as targets for antibacterial drugs,
CC   including anti-P. aeruginosa drugs, as templates for recombinant
CC   production of P. aeruginosa-derived peptides or polypeptides, as target
CC   components for diagnosis and/or treatment of P. aeruginosa-caused
CC   infection, and in detection of P. aeruginosa sequences or other sequences
CC   of Pseudomonas species using biochip technology. Sequences ABD01397-
CC   ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
SQ   Sequence 1050 BP; 162 A; 354 C; 348 G; 186 T; 0 U; 0 Other;

  Query Match             88.9%;  Score 16;  DB 11;  Length 1050;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCGGCGCAGGGGGG 18
              ||||||||||||||||
Db       1010 CGCCGGCGCAGGGGGG 1025


RESULT 6
AAL10608/c
ID   AAL10608 standard; cDNA; 374 BP.
XX
AC   AAL10608;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 3065.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US000798.
XX
PR   14-JAN-2000; 2000US-0176077P.
PR   14-MAR-2000; 2000US-0189167P.
PR   24-MAR-2000; 2000US-0192099P.
PR   29-MAR-2000; 2000US-0193480P.
PR   15-MAY-2000; 2000US-0205230P.
PR   09-JUN-2000; 2000US-0211315P.
PR   25-JUL-2000; 2000US-0220534P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer.
XX
PS   Claim 1; Page 569; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity
XX
SQ   Sequence 374 BP; 69 A; 109 C; 122 G; 68 T; 0 U; 6 Other;

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 374;
  Best Local Similarity   94.1%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||| |||||
Db        304 GCGCCGGCGCATGGGGG 288


RESULT 7
AAL17683/c
ID   AAL17683 standard; cDNA; 450 BP.
XX
AC   AAL17683;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 10140.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628-A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US000798.
XX
PR   14-JAN-2000; 2000US-0176077P.
PR   14-MAR-2000; 2000US-0189167P.
PR   24-MAR-2000; 2000US-0192099P.
PR   29-MAR-2000; 2000US-0193480P.
PR   15-MAY-2000; 2000US-0205230P.
PR   09-JUN-2000; 2000US-0211315P.
PR   25-JUL-2000; 2000US-0220534P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer.
XX
PS   Claim 1; Page 1809; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544-AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity
XX
SQ   Sequence 450 BP; 83 A; 138 C; 146 G; 83 T; 0 U; 0 Other;

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 450;
  Best Local Similarity   94.1%;  Pred. No. 2.7e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||| |||||
Db        260 GCGCCGGCGCATGGGGG 244


RESULT 8
AAC41286/c
ID   AAC41286 standard; DNA; 499 BP.
XX
AC   AAC41286;
```

XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 31332.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic; pathway;
KW promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.

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PR   27-AUG-1999;   99US-0151065P.
PR   27-AUG-1999;   99US-0151066P.
PR   27-AUG-1999;   99US-0151080P.
PR   30-AUG-1999;   99US-0151303P.
PR   31-AUG-1999;   99US-0151438P.
PR   01-SEP-1999;   99US-0151930P.
PR   07-SEP-1999;   99US-0152363P.
PR   10-SEP-1999;   99US-0153070P.
PR   13-SEP-1999;   99US-0153758P.
PR   15-SEP-1999;   99US-0154018P.
PR   16-SEP-1999;   99US-0154039P.
PR   20-SEP-1999;   99US-0154779P.
PR   22-SEP-1999;   99US-0155139P.
PR   23-SEP-1999;   99US-0155486P.
PR   24-SEP-1999;   99US-0155659P.
PR   28-SEP-1999;   99US-0156458P.
PR   29-SEP-1999;   99US-0156596P.
PR   04-OCT-1999;   99US-0157117P.
PR   05-OCT-1999;   99US-0157753P.
PR   06-OCT-1999;   99US-0157865P.
PR   07-OCT-1999;   99US-0158029P.
PR   08-OCT-1999;   99US-0158232P.
PR   12-OCT-1999;   99US-0158369P.
PR   13-OCT-1999;   99US-0159293P.
PR   13-OCT-1999;   99US-0159294P.
PR   13-OCT-1999;   99US-0159295P.
PR   14-OCT-1999;   99US-0159329P.
PR   14-OCT-1999;   99US-0159330P.
PR   14-OCT-1999;   99US-0159331P.
PR   14-OCT-1999;   99US-0159637P.
PR   14-OCT-1999;   99US-0159638P.
PR   18-OCT-1999;   99US-0159584P.
PR   21-OCT-1999;   99US-0160741P.
PR   21-OCT-1999;   99US-0160767P.
PR   21-OCT-1999;   99US-0160768P.
PR   21-OCT-1999;   99US-0160770P.
PR   21-OCT-1999;   99US-0160814P.
PR   21-OCT-1999;   99US-0160815P.
PR   22-OCT-1999;   99US-0160980P.
PR   22-OCT-1999;   99US-0160981P.
PR   22-OCT-1999;   99US-0160989P.
PR   25-OCT-1999;   99US-0161404P.
PR   25-OCT-1999;   99US-0161405P.
PR   25-OCT-1999;   99US-0161406P.
PR   26-OCT-1999;   99US-0161359P.
PR   26-OCT-1999;   99US-0161360P.
PR   26-OCT-1999;   99US-0161361P.
PR   28-OCT-1999;   99US-0161920P.
PR   28-OCT-1999;   99US-0161992P.
PR   28-OCT-1999;   99US-0161993P.
PR   29-OCT-1999;   99US-0162142P.

  Query Match             85.6%;  Score 15.4;  DB 3;  Length 499;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||| ||||||||||||
Db        166 GCGCAGGCGCAGGGGGG 150


RESULT 9
ACN80806/c
ID   ACN80806 standard; DNA; 513 BP.
XX
AC   ACN80806;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Breast cancer related marker, seq id 1956.
XX
KW   Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS   Homo sapiens.
XX
PN   US2003099974-A1.
XX
PD   29-MAY-2003.
XX
PF   18-JUL-2002; 2002US-00198846.
XX
PR   18-JUL-2001; 2001US-0306220P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2003-787014/74.
XX
PT   Novel isolated polypeptide associated with breast cancer, useful for
PT   detecting presence of polypeptide in sample, as a marker for breast
PT   cancer.
XX
PS   Disclosure; SEQ ID NO 1956; 36pp; English.
XX
CC   The invention relates to an isolated polypeptide (I) associated with
CC   breast cancer which is encoded by a nucleic acid molecule comprising a
CC   nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC   the polypeptide of the invention. The activity of the polypeptide of the
CC   invention may be described as cytostatic. The antibody is useful for
CC   detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC   invention are useful in the detection of breast tumours. (I) is useful as
CC   a marker for breast cancer and in breast cancer therapy. Sequences given
CC   in records ACN78851-ACN92934 represent nucleic acid markers associated
CC   with breast cancer. Note: The sequence listing does not form part of the
CC   specification but may be obtained in electronic format from the USPTO web
CC   site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ   Sequence 513 BP; 93 A; 152 C; 163 G; 92 T; 0 U; 13 Other;

  Query Match             85.6%;  Score 15.4;  DB 11;  Length 513;
  Best Local Similarity   94.1%;  Pred. No. 2.6e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||||| |||||
Db        322 GCGCCGGCGCATGGGGG 306


RESULT 10
ADL85306/c
ID   ADL85306 standard; DNA; 564 BP.
XX
AC   ADL85306;
XX
DT   20-MAY-2004  (first entry)
XX
DE   DNA up-regulated in murine common lymphoid myeloid cells SeqID 1699.
XX
KW   gene potential; multi-lineage; cell commitment; haematopoietic stem cell;
KW   HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP;
KW   common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
XX
OS   Mus sp.
XX
PN   WO2003093445-A2.
XX
PD   13-NOV-2003.
XX
PF   05-MAY-2003; 2003WO-US014114.
XX
PR   03-MAY-2002; 2002US-0377383P.
XX
PA   (STOW-) STOWERS INST MEDICAL RES.
XX
PI   Li L;
```

XX
DR WPI; 2004-022656/02.
XX
PT Classifying an unknown multi-lineage affiliated gene comprises isolating
PT expressed nucleic acid sequences from the discrete cell sub-populations.
XX
PS Claim 9; SEQ ID NO 1699; 123pp; English.
XX
CC This invention relates to a novel method for predicting gene potential by
CC associating nucleic acid sequences of unknown function with particular
CC sub-population profiles. Specifically, it refers to classifying an
CC unknown multi-lineage affiliated gene by collecting hybridisation data to
CC develop a gene expression map, in order to determine the discrete sub-
CC population where it is expressed. The present invention describes methods
CC for predicting the lineage commitment of genes associated with the self-
CC renewing haematopoietic (blood) stem cells (HSCs), as well as the non-
CC self renewing multipotent progenitors (MPPs), common lymphoid progenitors
CC (CLPs) and common myeloid progenitors (CMPs), which are collectively
CC referred to as bone marrow stem cells populations. As such, these methods
CC can be used to identify associated multi-lineage affiliated genes and
CC hence the underlying molecular mechanisms in physiological haematopoietic
CC development. This polynucleotide sequence is DNA associated with a murine
CC CMP sub population of cells of the invention.
XX
SQ Sequence 564 BP; 89 A; 173 C; 150 G; 144 T; 0 U; 8 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 564;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGG 17
||| |||||||||||||
Db 125 TGCCCCGGCGCAGGGGG 109

RESULT 11
ADL85307/c
ID ADL85307 standard; DNA; 564 BP.
XX
AC ADL85307;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1700.
XX
KW gene potential; multi-lineage; cell commitment; haematopoietic stem cell;
KW HSC; multipotent progenitor; MPP; common lymphoid progenitor; CLP;
KW common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
XX
OS Mus sp.
XX
PN WO2003093445-A2.
XX
PD 13-NOV-2003.
XX
PF 05-MAY-2003; 2003WO-US014114.
XX
PR 03-MAY-2002; 2002US-0377383P.
XX
PA (STOW-) STOWERS INST MEDICAL RES.
XX
PI Li L;
XX
DR WPI; 2004-022656/02.
XX
PT Classifying an unknown multi-lineage affiliated gene comprises isolating
PT expressed nucleic acid sequences from the discrete cell sub-populations.
XX
PS Claim 9; SEQ ID NO 1700; 123pp; English.
XX
CC This invention relates to a novel method for predicting gene potential by
CC associating nucleic acid sequences of unknown function with particular
CC sub-population profiles. Specifically, it refers to classifying an
CC unknown multi-lineage affiliated gene by collecting hybridisation data to
CC develop a gene expression map, in order to determine the discrete sub-
CC population where it is expressed. The present invention describes methods
CC for predicting the lineage commitment of genes associated with the self-
CC renewing haematopoietic (blood) stem cells (HSCs), as well as the non-
CC self renewing multipotent progenitors (MPPs), common lymphoid progenitors
CC (CLPs) and common myeloid progenitors (CMPs), which are collectively
CC referred to as bone marrow stem cells populations. As such, these methods
CC can be used to identify associated multi-lineage affiliated genes and
CC hence the underlying molecular mechanisms in physiological haematopoietic
CC development. This polynucleotide sequence is DNA associated with a murine
CC CMP sub population of cells of the invention.
XX
SQ Sequence 564 BP; 89 A; 173 C; 150 G; 144 T; 0 U; 8 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 564;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGG 17
||| |||||||||||||
Db 125 TGCCCCGGCGCAGGGGG 109

RESULT 12
ACH71251/c
ID ACH71251 standard; DNA; 597 BP.
XX
AC ACH71251;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #4446.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 15; SEQ ID NO 4446; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above- mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 597 BP; 81 A; 242 C; 154 G; 120 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 597;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCCGGCGCAGGGGGG 18
|||| ||||||||||||
Db 212 GCGCGGGCGCAGGGGGG 196

RESULT 13
ACN86723/c
ID ACN86723 standard; DNA; 664 BP.
XX
AC ACN86723;
XX
DT 02-DEC-2004 (first entry)
XX
DE Breast cancer related marker, seq id 7873.
XX
KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS Homo sapiens.
XX
PN US2003099974-A1.
XX
PD 29-MAY-2003.
XX
PF 18-JUL-2002; 2002US-00198846.
XX
PR 18-JUL-2001; 2001US-0306220P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX
DR WPI; 2003-787014/74.
XX
PT Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.
XX
PS Disclosure; SEQ ID NO 7873; 36pp; English.
XX
CC The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ Sequence 664 BP; 134 A; 179 C; 204 G; 118 T; 0 U; 29 Other;

Query Match 85.6%; Score 15.4; DB 11; Length 664;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCCGGCGCAGGGGGG 18
|||| ||||||||||||
Db 295 GCGCCGGCGCATGGGGG 279

RESULT 14
ADJ11795/c
ID ADJ11795 standard; DNA; 681 BP.
XX
AC ADJ11795;
XX
DT 20-MAY-2004 (first entry)
XX
DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 431.
XX
KW rice; gene; ss; post-transcriptional gene silencing; PTGS; plant;
KW trans-activation; cereal; plant-viral interaction.
XX
OS Oryza sp.
XX
PN US2003135888-A1.
XX
PD 17-JUL-2003.
XX
PF 26-SEP-2002; 2002US-00259165.
XX
PR 26-SEP-2001; 2001US-0325277P.
PR 27-MAR-2002; 2002US-0368327P.
PR 04-APR-2002; 2002US-0370620P.
XX
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
XX
PI Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;
XX
DR WPI; 2003-829655/77.
DR P-PSDB; ADJ11796.
XX
PT New polynucleotide, useful for modulating gene expression within a cell
PT by posttranscriptional gene silencing.
XX
PS Example 15; SEQ ID NO 431; 79pp; English.
XX
CC This invention relates to a novel method for identifying isolated
CC polynucleotides that are modulated by post-transcriptional gene silencing
CC (PTGS). Specifically, it refers to the regulation of gene expression in

```
CC   plants via PTGS and the trans-activation of homologous genes due to
CC   increased RNA degradation. The present invention describes clusters of
CC   polynucleotides from cereals, in particular rice, as well as homologues
CC   and the polypeptide sequences derived thereof, where gene expression is
CC   altered in response to PTGS. As such, the elucidation of gene silencing
CC   mechanisms can lead to more efficiently expressed transgenes, and can
CC   also improve the understanding of plant-viral interactions and targeting
CC   the suppression of specific plant genes. This polynucleotide sequence is
CC   a rice cDNA sequence where expression is modulated by gene silencing,
CC   given in an exemplification of the invention. NOTE: This sequence does
CC   not appear in the printed specification but has been obtained in
CC   electronic format from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID=20030135888.
XX
SQ   Sequence 681 BP; 80 A; 246 C; 253 G; 102 T; 0 U; 0 Other;

  Query Match             85.6%;  Score 15.4;  DB 11;  Length 681;
  Best Local Similarity   94.1%;  Pred. No. 2.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGG 17
              ||||||||| |||||||
Db        637 TGCGCCGGCACAGGGGG 621


RESULT 15
ADJ11463/c
ID   ADJ11463 standard; DNA; 684 BP.
XX
AC   ADJ11463;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Rice DNA modulated by post-transcriptional gene silencing SeqID 99.
XX
KW   rice; gene; ds; post-transcriptional gene silencing; PTGS; plant;
KW   trans-activation; cereal; plant-viral interaction.
XX
OS   Oryza sp.
XX
PN   US2003135888-A1.
XX
PD   17-JUL-2003.
XX
PF   26-SEP-2002; 2002US-00259165.
XX
PR   26-SEP-2001; 2001US-0325277P.
PR   27-MAR-2002; 2002US-0368327P.
PR   04-APR-2002; 2002US-0370620P.
XX
PA   (ZHUT/) ZHU T.
PA   (WANG/) WANG X.
PA   (CHAN/) CHANG H.
PA   (BRIG/) BRIGGS S P.
PA   (COOP/) COOPER B.
PA   (GLAZ/) GLAZEBROOK J.
PA   (GOFF/) GOFF S A.
PA   (KATA/) KATAGIRI F.
PA   (KREP/) KREPS J.
PA   (MOUG/) MOUGHAMER T.
PA   (PROV/) PROVART N.
PA   (RICK/) RICKE D.
XX
PI   Zhu T,  Wang X,  Chang H,  Briggs SP,  Cooper B,  Glazebrook J;
PI   Goff SA,  Katagiri F,  Kreps J,  Moughamer T,  Provart N,  Ricke D;
XX
DR   WPI; 2003-829655/77.
DR   P-PSDB; ADJ11464.
XX
PT   New polynucleotide, useful for modulating gene expression within a cell
PT   by posttranscriptional gene silencing.
XX
PS   Claim 1; SEQ ID NO 99; 79pp; English.
XX
CC   This invention relates to a novel method for identifying isolated
CC   polynucleotides that are modulated by post-transcriptional gene silencing
CC   (PTGS). Specifically, it refers to the regulation of gene expression in
CC   plants via PTGS and the trans-activation of homologous genes due to
CC   increased RNA degradation. The present invention describes clusters of
CC   polynucleotides from cereals, in particular rice, as well as homologues
CC   and the polypeptide sequences derived thereof, where gene expression is
CC   altered in response to PTGS. As such, the elucidation of gene silencing
CC   mechanisms can lead to more efficiently expressed transgenes, and can
CC   also improve the understanding of plant-viral interactions and targeting
CC   the suppression of specific plant genes. This polynucleotide sequence is
CC   a rice DNA sequence where expression is modulated by gene silencing,
CC   given in an exemplification of the invention. NOTE: This sequence does
CC   not appear in the printed specification but has been obtained in
CC   electronic format from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID=20030135888.
XX
SQ   Sequence 684 BP; 81 A; 246 C; 254 G; 103 T; 0 U; 0 Other;

  Query Match             85.6%;  Score 15.4;  DB 11;  Length 684;
  Best Local Similarity   94.1%;  Pred. No. 2.5e+03;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGG 17
              ||||||||| |||||||
Db        637 TGCGCCGGCACAGGGGG 621


Search completed: April 29, 2005, 06:26:04
Job time : 186.527 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1687.62 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-17
Perfect score: 18
Sequence: 1 tgcgccggcgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18	100.0	493	8	AQ834558	HS_5262_B
c 2	17	94.4	800	4	BI824249	BI824249 603040633
3	17	94.4	1015	5	BQ722659	BQ722659 AGENCOURT
c 4	17	94.4	1417	5	BU540484	BU540484 AGENCOURT
5	17	94.4	1597	7	CN248554	CN248554 EST014461
c 6	16.6	92.2	630	9	CNS01T3H	AL166022 Tetraodon
7	16.6	92.2	687	9	CNS026IH	AL183410 Tetraodon
c 8	16.4	91.1	107	4	BM441533	BM441533 EBma05_SQ
c 9	16.4	91.1	419	6	CA003765	CA003765 HS15H23r
c 10	16.4	91.1	438	6	CA389497	CA389497 cs09h05.y
c 11	16.4	91.1	454	7	CK124280	CK124280 BES182410
c 12	16.4	91.1	487	9	CL809531	CL809531 OR_CBa002
c 13	16.4	91.1	524	7	CV060996	CV060996 BNEL63g12
c 14	16.4	91.1	529	9	CL726375	CL726375 OR_BBa005
c 15	16.4	91.1	532	9	CL720522	CL720522 OR_BBa004
c 16	16.4	91.1	554	7	CV058883	CV058883 BNEL42a7
c 17	16.4	91.1	569	7	CV062273	CV062273 BNEL78c1
c 18	16.4	91.1	570	6	CA006705	CA006705 HU05H16r
c 19	16.4	91.1	574	7	CV054681	CV054681 BNEL112b3
c 20	16.4	91.1	574	7	CV058059	CV058059 BNEL33h4
c 21	16.4	91.1	574	7	CV062564	CV062564 BNEL80d9
c 22	16.4	91.1	574	7	CV063117	CV063117 BNEL86g8
c 23	16.4	91.1	577	6	CA757679	CA757679 OE06F11-T
24	16.4	91.1	583	9	CG852075	CG852075 ZMMBBb034
c 25	16.4	91.1	589	7	CV062852	CV062852 BNEL83g5
c 26	16.4	91.1	602	7	CV058190	CV058190 BNEL35c8
c 27	16.4	91.1	608	7	CV517724	CV517724 0089P0004
c 28	16.4	91.1	617	7	CV056834	CV056834 BNEL21b10
c 29	16.4	91.1	619	7	CV056063	CV056063 BNEL13E4
c 30	16.4	91.1	631	7	CV060804	CV060804 BNEL61d3
c 31	16.4	91.1	660	5	BQ465952	BQ465952 HT01C12T
c 32	16.4	91.1	671	1	AL508223	AL508223 AL508223
c 33	16.4	91.1	676	5	BQ466861	BQ466861 HS01N03T
34	16.4	91.1	791	6	CB961213	CB961213 AGENCOURT
35	16.4	91.1	797	6	CB988944	CB988944 AGENCOURT
c 36	16.4	91.1	840	4	BI951157	BI951157 HVSME1002
37	16.4	91.1	867	5	BX337000	BX337000 BX337000
c 38	16.4	91.1	908	9	AG430840	AG430840 Mus muscu
c 39	16.4	91.1	913	4	BG169129	BG169129 602320581
40	16.4	91.1	917	9	CG342398	CG342398 OGWMK07TV
41	16.4	91.1	919	8	BZ824306	BZ824306 PUGBF62TD
c 42	16.4	91.1	921	2	BE454364	BE454364 HVSMEh009
c 43	16.4	91.1	929	5	BQ643095	BQ643095 AGENCOURT
c 44	16.4	91.1	950	9	CG293894	CG293894 OGWGP15TH
45	16.4	91.1	960	9	CNS03ZKW	AL267737 Tetraodon

ALIGNMENTS

RESULT 1
AQ834558/c
LOCUS AQ834558 493 bp DNA linear GSS 27-AUG-1999
DEFINITION HS_5262_B1_G02_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=838 Col=3 Row=N, genomic survey sequence.
ACCESSION AQ834558
VERSION AQ834558.1 GI:5800620
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 493)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 838 row: N column: 3
Seq primer: T7
Class: BAC ends
High quality sequence stop: 493.
FEATURES Location/Qualifiers
source 1. .493
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=838 Col=3 Row=N"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGCCGGCGCAGGGGGG 18
||||||||||||||||||
Db 200 TGCGCCGGCGCAGGGGGG 183

RESULT 2
BI824249/c
LOCUS BI824249 800 bp mRNA linear EST 04-OCT-2001
DEFINITION 603040633F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181224 5', mRNA sequence.
ACCESSION BI824249
VERSION BI824249.1 GI:15935799
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11452 row: b column: 09
High quality sequence start: 2
High quality sequence stop: 568.
FEATURES Location/Qualifiers
source 1. .800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5181224"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.4%; Score 17; DB 4; Length 800;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGCCGGCGCAGGGGGG 18
|||||||||||||||||
Db 666 GCGCCGGCGCAGGGGGG 650

RESULT 3
BQ722659
LOCUS BQ722659 1015 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8219609 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6188410 5', mRNA sequence.
ACCESSION BQ722659
VERSION BQ722659.1 GI:21861556
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1015)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13583 row: p column: 11
High quality sequence stop: 262.
FEATURES Location/Qualifiers
source 1. .1015
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6188410"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

ORIGIN

Query Match 94.4%; Score 17; DB 5; Length 1015;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGCCGGCGCAGGGGGG 18
|||||||||||||||||
Db 943 GCGCCGGCGCAGGGGGG 959

RESULT 4
BU540484/c
LOCUS BU540484 1417 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10325169 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6571942 5', mRNA sequence.
ACCESSION BU540484
VERSION BU540484.1 GI:22850925
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1417)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2763  row: d  column: 22
            High quality sequence start: 57
            High quality sequence stop: 392.
FEATURES             Location/Qualifiers
     source          1. .1417
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6571942"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_18"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             94.4%;  Score 17;  DB 5;  Length 1417;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||||||||||
Db        852 GCGCCGGCGCAGGGGGG 836


RESULT 5
CN248554
LOCUS       CN248554                1597 bp    mRNA    linear   EST 09-APR-2004
DEFINITION  EST014461 Mycelium and yeast cells from Paracoccidioides
            brasiliensis Paracoccidioides brasiliensis cDNA, mRNA sequence.
ACCESSION   CN248554
VERSION     CN248554.1  GI:46352298
KEYWORDS    EST.
SOURCE      Paracoccidioides brasiliensis
  ORGANISM  Paracoccidioides brasiliensis
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Paracoccidioides.
REFERENCE   1  (bases 1 to 1597)
  AUTHORS   Felipe,M.S.S., Carvalho,M.J.A., Andrade,R.V., Arraes,F.B.M.,
            Simoes,I.C., Andrade,E.V., Maranhao,A.Q., Torres,F.A.G.:
            Jesuino,R.S.A., Kyaw,C.M., Moraes,L.M.P., Nicola,A., Pereira,M.,
            Silva-Pereira,I., Anjos,D.A.S., Sandes,E.F.O., Inoue,M.K.,
            Walter,M.E.M.T., Soares,C.M.A. and Brigido,M.M.
  TITLE     Metabolic features of Paracoccidioides brasiliensis cell
            differentiation as accessed by transcriptome analysis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Felipe MSS
            Laboratory of Molecular Biology
            Institute of Biology - University of Brasilia
            Campus Universitario, Asa Norte, Brasilia, DF 70910-900, BRA
            Tel: 55 61 307 2423
            Fax: 55 61 349 8411
            Email: msueli@unb.br
            Seq primer: T7 Sequencing primer.
FEATURES             Location/Qualifiers
     source          1. .1597
                     /organism="Paracoccidioides brasiliensis"
                     /mol_type="mRNA"
                     /strain="Pb01"
                     /db_xref="taxon:121759"
                     /clone_lib="Mycelium and yeast cells from Paracoccidioides
                     brasiliensis"
                     /note="Pb Lambda Zap Express Library"
ORIGIN

  Query Match             94.4%;  Score 17;  DB 7;  Length 1597;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||||||||||||||||
Db        975 GCGCCGGCGCAGGGGGG 991


RESULT 6
CNS01T3H/c
LOCUS       CNS01T3H                630 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            194E11 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL166022
VERSION     AL166022.1  GI:7803760
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 630)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="194E11"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG194AC06LP1~end : T7"
ORIGIN

  Query Match             92.2%;  Score 16.6;  DB 9;  Length 630;
  Best Local Similarity   94.1%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||||||||||:|
Db        152 GCGCCGGCGCAGGGGSG 136


RESULT 7
CNS026IH
LOCUS       CNS026IH                  687 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            241C17 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL183410
VERSION     AL183410.1  GI:7821514
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 687)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .687
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="241C17"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG241AB09SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             92.2%;  Score 16.6;  DB 9;  Length 687;
  Best Local Similarity   94.1%;  Pred. No. 4.4e+03;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||||||||||:||
Db        507 GCGCCGGCGCAGGGSGG 523


RESULT 8
BM441533/c
LOCUS       BM441533                  107 bp    mRNA    linear   EST 23-JUL-2002
DEFINITION  EBma05_SQ004_L14_R maternal, 12 DPA, no treatment, cv Optic, EBma05
            Hordeum vulgare subsp. vulgare cDNA clone EBma05_SQ004_L14 5', mRNA
            sequence.
ACCESSION   BM441533
VERSION     BM441533.2  GI:21942320
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 107)
  AUTHORS   Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
            Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
  TITLE     Development of Barley Transcriptome Resources
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 1, 2002 this sequence version replaced gi:18472308.
            Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk
            All sequence has a Phred quality score of 20 or over
            Seq primer: M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .107
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Optic"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="EBma05_SQ004_L14"
                     /tissue_type="maternal"
                     /dev_stage="12 DPA"
                     /lab_host="DH10B"
                     /clone_lib="maternal, 12 DPA, no treatment, cv Optic,
                     EBma05"
                     /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
                     Non-normalised library, directionally cloned into pSPORT1.
                     Derived from maternal tissue dissected from developing
                     grains (12 days post anthesis) in glasshouse grown barley
                     plants.  Developed as part of the barley transcriptome
                     resources of BBSRC/SEERAD funded cereal IGF (Investigating
                     Gene Function) project."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 4;  Length 107;
  Best Local Similarity   94.4%;  Pred. No. 6.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||||||| ||||||
Db         96 TGCGCCGGCGCCGGGGGG 79


RESULT 9
CA003765/c
LOCUS       CA003765                  419 bp    mRNA    linear   EST 23-OCT-2002
DEFINITION  HS15H23r HS Hordeum vulgare subsp. vulgare cDNA clone HS15H23
            5-PRIME, mRNA sequence.
ACCESSION   CA003765
VERSION     CA003765.1  GI:24280747
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 419)
  AUTHORS   Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
            Graner,A.
  TITLE     Barley ESTs from germinating seeds
```

```
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Stein Nils
            Molecular Markers Group, Department Genbank
            Institute of Plant Genetics and Crop Plant Research (IPK)
            Corrensstr. 3, 06466, Gatersleben, Germany
            Tel: 039482-5522
            Fax: 039482-5595
            Email: stein@ipk-gatersleben.de
            Insert Length: 419   Std Error: 0.00
            Plate: 15  row: H  column: 23
            Seq primer: M13rev.
FEATURES             Location/Qualifiers
     source          1. .419
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="GABI:258977"
                     /db_xref="taxon:112509"
                     /clone="HS15H23"
                     /tissue_type="embryo + scutellum"
                     /dev_stage="0-16 hours after imbibition"
                     /lab_host="XL10-Gold"
                     /clone_lib="HS"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
                     cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
                     artefact caused by the kit, in most cases the EcoRI site
                     is NOT present, as well as the EcoRIadapter used for
                     cloning. To excise the insert, restriction sites upstream
                     EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also
                     due to the cloning system used Blue/white selection for
                     recombinats is not 100% reliable."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 419;
  Best Local Similarity   94.4%;  Pred. No. 5.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||||||| ||||||
Db        397 TGCGCCGGCGCCGGGGGG 380


RESULT 10
CA389497/c
LOCUS       CA389497                438 bp    mRNA    linear   EST 06-NOV-2002
DEFINITION  cs09h05.y1 Human Retinal pigment epithelium/choroid cDNA
            (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs09h05
            5', mRNA sequence.
ACCESSION   CA389497
VERSION     CA389497.1  GI:24719710
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 438)
  AUTHORS   Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
            Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
  TITLE     Expressed sequence tag analysis of human RPE/choroid for the
            NEIBank Project: Over 6000 non-redundant transcripts, novel genes
            and splice variants
  JOURNAL   Mol. Vis. 8 (4), 205-220 (2002)
  MEDLINE   22103460
   PUBMED   12107410
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 09  row: h  column: 05
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .438
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="cs09h05"
                     /tissue_type="RPE/choroid"
                     /dev_stage="Adult"
                     /lab_host="EMDH10B"
                     /clone_lib="Human Retinal pigment epithelium/choroid cDNA
                     (Un-normalized, unamplified): cs"
                     /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
                     eyes (75-80 years old) yielded approximately 600 mg of
                     dissected RPE/choroid tissue.  This in turn yielded 340 ug
                     of total RNA and 7 ug of mRNA. A directionally cloned cDNA
                     library in the pCMVSPORT6 vector was constructed at Life
                     Technologies (Rockville, MD; now part of Invitrogen Corp),
                     essentially following the protocols of the SuperScript
                     Plasmid System (Invitrogen Corp.
                     <http://www.invitrogen.com/>). The library code
                     designation was cs. For this library, cDNA inserts were
                     cloned into the NotI/MluI sites of the vector. EST
                     analysis was performed on the unamplified library at the
                     NIH Intramural Sequencing Center (NISC)."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 6;  Length 438;
  Best Local Similarity   94.4%;  Pred. No. 5.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              | ||||||||||||||||
Db        149 TCCGCCGGCGCAGGGGGG 132


RESULT 11
CK124280/c
LOCUS       CK124280                454 bp    mRNA    linear   EST 01-MAR-2004
DEFINITION  BES1824108d24 BES1824 Hordeum vulgare subsp. vulgare cDNA clone
            MPMGp2010D248 5-PRIME, mRNA sequence.
ACCESSION   CK124280
VERSION     CK124280.1  GI:44807282
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Kramer,A., Feilner,T., Possling,A., Radchuk,V., Weschke,W.,
            Buerkle,L. and Kersten,B.
  TITLE     Application of the protein microarray technology for the
            identification of expression library derived target proteins for
            barley protein kinase CK2
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Birgit Kersten* and Winfriede Weschke**
            *Plant Protein Chip Group, Department Lehrach, **Department
            Molecular Genetics, Gene Expression Group
            *Max-Planck-Institute for Molecular Genetics, **Institute of Plant
            Genetics and Crop Plant Research Gatersleben
            *Ihnestr. 73 , D-14195 Berlin, Germany, **Corrensstrasse 3, D-06466
            Gatersleben, Germany
            Tel: *+49(0)30/84131648,**+49(0)394825500
            Fax: *+49(0)30/84131128,**+49(0)394825237
            Email: *kersten@molgen.mpg.de, **weschke@ipk-gatersleben.de
            Insert Length: 454   Std Error: 0.00
            Plate: 8  row: D  column: 24
            Seq primer: pQE65.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
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                     /cultivar="barke"
                     /sub_species="vulgare"
                     /db_xref="GABI:945085"
                     /db_xref="taxon:112509"
                     /clone="MPMGp2010D248"
                     /tissue_type="embryosac"
                     /dev_stage="0-10 DAF (days after flowering)"
                     /lab_host="E. coli, SCS-1/pSE111"
                     /clone_lib="BES1824"
                     /note="Vector: pQE30NST (AF074376); Site_1: SalI; Site_2:
                     NotI; 0-10 DAF (days after flowering), cDNA synthesis
                     using pBluescript II XR cDNA-library construction kit
                     (Stratagen) with an oligo(dT)-primer containing NotI
                     restriction site and a SalI adapter (Invitrogen). The main
                     library of 21500 clones was rearrayed into the sublibrary
                     BES 1824 containing 4100 putative expression clones. Note:
                     Due to a cloning artefact caused by the kit, in most cases
                     the SalI site is NOT present, as well as the SalI Adapter
                     used for cloning. To excise the insert, restriction sites
                     upstream SalI should be used (e.g. BamHI). Average insert
                     size is 1 kb. Library generation and sequencing was
                     granted in context of GABI; data are also accessible at
                     https://gabi.rzpd.de"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 7;  Length 454;
  Best Local Similarity   94.4%;  Pred. No. 5.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              ||||||||||| ||||||
Db        213 TGCGCCGGCGCCGGGGGG 196


RESULT 12
CL809531/c
LOCUS       CL809531                487 bp    DNA     linear   GSS 09-AUG-2004
DEFINITION  OR_CBa0024F19.f OR_CBa Oryza rufipogon genomic clone OR_CBa0024F19
            5', genomic survey sequence.
ACCESSION   CL809531
VERSION     CL809531.1  GI:51047583
KEYWORDS    GSS.
SOURCE      Oryza rufipogon
  ORGANISM  Oryza rufipogon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 487)
  AUTHORS   Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
            Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
            Wing,R.
  TITLE     OMAP project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0024  row: F  column: 19
            Seq primer: TAA TAC GAC TCA CTA TAG GG
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Oryza rufipogon"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4529"
                     /clone="OR_CBa0024F19"
                     /tissue_type="young leaves"
                     /dev_stage="2 week old seedlings"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OR_CBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
                     drk treated 36 hrs before harvest"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 487;
  Best Local Similarity   94.4%;  Pred. No. 5.6e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||||||||||||||| |
Db        359 TGCGCCGGCGCAGGGGAG 342


RESULT 13
CV060996/c
LOCUS       CV060996                524 bp    mRNA    linear   EST 24-AUG-2004
DEFINITION  BNEL63g12 Barley EST endosperm library Hordeum vulgare subsp.
            vulgare cDNA clone BNEL63g12 5' similar to P0028G04.23, mRNA
            sequence.
ACCESSION   CV060996
VERSION     CV060996.1  GI:51524135
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 524)
  AUTHORS   Ali,S, Holloway,B. and Taylor,W.C.
  TITLE     Normalisation of cereal endosperm EST libraries for structural and
            functional genomic analysis
  JOURNAL   Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT     Contact: Bill Taylor
            Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry.
            CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
            Tel: 61 2 6246 5223
            Fax: 61 2 6246 5000
            Email: Bill.Taylor@csiro.au
            Seq primer: M13 reverse primer
            High quality sequence stop: 524.
FEATURES             Location/Qualifiers
     source          1. .524
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="Himalaya"
                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="BNEL63g12"
                     /tissue_type="endosperm"
                     /dev_stage="developing endosperm tissue 10, 12, 15 dpa
                     (days post anthesis)"
                     /lab_host="DH10B (Life Technology)"
                     /clone_lib="Barley EST endosperm library"
                     /note="Vector: _ZipLox; Site_1: Sal I; Site_2: Not I; mRNA
                     was prepared from endosperm tissues of the barley cultivar
                     Himalaya. cDNA was synthesised from pooled 10, 12, and 15
                     dpa endosperm using Not I-oligo(dT)18 primer/adapter
                     (Pharmacia Biotech), and then ligated to the Sal I-Not I
                     site of _ZipLox vector (Life Technology) after adding a
                     Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan
                     Ali and Bill Taylor."
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 7;  Length 524;
  Best Local Similarity   94.4%;  Pred. No. 5.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db        333 TGCGCCGGCGCCGGGGGG 316


RESULT 14
CL726375/c
LOCUS       CL726375                529 bp    DNA     linear   GSS 26-JUL-2004
DEFINITION  OR_BBa0056K14.f OR_BBa Oryza rufipogon genomic clone OR_BBa0056K14
            5', genomic survey sequence.
ACCESSION   CL726375
VERSION     CL726375.1  GI:50623473
KEYWORDS    GSS.
SOURCE      Oryza rufipogon
  ORGANISM  Oryza rufipogon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
            Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
  TITLE     OMAP Project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Insert Length: 161   Std Error: 0.00
            Plate: 0056  row: K  column: 14
            Seq primer: TAA TAC GAC TCA CTA TAG GG
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /organism="Oryza rufipogon"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4529"
                     /clone="OR_BBa0056K14"
                     /tissue_type="young leaves"
                     /lab_host="DH10B-T1 phage resistant"
                     /clone_lib="OR_BBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 529;
  Best Local Similarity   94.4%;  Pred. No. 5.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||||||||||||| |
Db        380 TGCGCCGGCGCAGGGGAG 363


RESULT 15
CL720522/c
LOCUS       CL720522                532 bp    DNA     linear   GSS 26-JUL-2004
DEFINITION  OR_BBa0048J24.f OR_BBa Oryza rufipogon genomic clone OR_BBa0048J24
            5', genomic survey sequence.
ACCESSION   CL720522
VERSION     CL720522.1  GI:50611811
KEYWORDS    GSS.
SOURCE      Oryza rufipogon
  ORGANISM  Oryza rufipogon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 532)
  AUTHORS   Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
            Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
  TITLE     OMAP Project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Insert Length: 161   Std Error: 0.00
            Plate: 0048  row: J  column: 24
            Seq primer: TAA TAC GAC TCA CTA TAG GG
            Class: BAC ends.
FEATURES             Location/Qualifiers
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                     /organism="Oryza rufipogon"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4529"
                     /clone="OR_BBa0048J24"
                     /tissue_type="young leaves"
                     /lab_host="DH10B-T1 phage resistant"
                     /clone_lib="OR_BBa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             91.1%;  Score 16.4;  DB 9;  Length 532;
  Best Local Similarity   94.4%;  Pred. No. 5.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db        381 TGCGCCGGCGCAGGGGAG 364


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	16.4	91.1	448	4	US-09-270-767-1195	Sequence 1195, Ap
c	2	16.4	91.1	448	4	US-09-270-767-16477	Sequence 16477, A
	3	16	88.9	963	4	US-09-252-991A-7939	Sequence 7939, Ap
	4	16	88.9	1050	4	US-09-252-991A-7799	Sequence 7799, Ap
c	5	15.4	85.6	900	4	US-10-101-464A-282	Sequence 282, App
c	6	15.4	85.6	1008	4	US-09-640-211A-329	Sequence 329, App
c	7	15.4	85.6	2478	4	US-10-101-464A-859	Sequence 859, App
	8	15.4	85.6	9499	4	US-09-949-016-15514	Sequence 15514, A
c	9	15.4	85.6	16011	4	US-09-600-319-3	Sequence 3, Appli
	10	15.4	85.6	26289	4	US-09-902-540-1210	Sequence 1210, Ap
c	11	15.4	85.6	154746	4	US-09-827-688-8	Sequence 8, Appli
	12	15	83.3	1771	4	US-09-902-540-6323	Sequence 6323, Ap
	13	15	83.3	2178	4	US-09-902-540-392	Sequence 392, App
	14	14.8	82.2	246	4	US-09-382-552-59	Sequence 59, Appl
	15	14.8	82.2	426	4	US-09-252-991A-3760	Sequence 3760, Ap
c	16	14.8	82.2	450	4	US-09-585-645A-22	Sequence 22, Appl
c	17	14.8	82.2	526	4	US-09-949-016-191144	Sequence 191144,
	18	14.8	82.2	774	4	US-09-489-039A-1478	Sequence 1478, Ap
c	19	14.8	82.2	885	4	US-09-252-991A-16564	Sequence 16564, A
c	20	14.8	82.2	1110	4	US-09-489-039A-6658	Sequence 6658, Ap
	21	14.8	82.2	1169	4	US-09-620-312D-951	Sequence 951, App
c	22	14.8	82.2	1230	4	US-09-489-039A-6246	Sequence 6246, Ap
c	23	14.8	82.2	1251	4	US-09-252-991A-16454	Sequence 16454, A
	24	14.8	82.2	1251	4	US-09-902-540-8793	Sequence 8793, Ap
	25	14.8	82.2	1256	3	US-09-318-448-42	Sequence 42, Appl
	26	14.8	82.2	1269	4	US-09-252-991A-16036	Sequence 16036, A
	27	14.8	82.2	1273	3	US-09-318-448-45	Sequence 45, Appl
	28	14.8	82.2	1275	3	US-09-318-448-41	Sequence 41, Appl
c	29	14.8	82.2	1294	4	US-09-735-846-13	Sequence 13, Appl
	30	14.8	82.2	1473	4	US-09-252-991A-13784	Sequence 13784, A
	31	14.8	82.2	1500	4	US-09-252-991A-13688	Sequence 13688, A
	32	14.8	82.2	1581	4	US-09-902-540-8068	Sequence 8068, Ap
c	33	14.8	82.2	1749	3	US-09-516-914-22	Sequence 22, Appl
	34	14.8	82.2	1908	3	US-09-318-448-36	Sequence 36, Appl
	35	14.8	82.2	1953	4	US-09-252-991A-3804	Sequence 3804, Ap
c	36	14.8	82.2	2283	4	US-09-949-016-4804	Sequence 4804, Ap
c	37	14.8	82.2	2289	4	US-09-489-039A-2837	Sequence 2837, Ap
	38	14.8	82.2	2291	4	US-09-902-540-376	Sequence 376, App
	39	14.8	82.2	2355	4	US-09-252-991A-3845	Sequence 3845, Ap
	40	14.8	82.2	2451	4	US-09-489-039A-3349	Sequence 3349, Ap
c	41	14.8	82.2	2515	4	US-09-244-805-10	Sequence 10, Appl
c	42	14.8	82.2	2523	4	US-09-489-039A-3473	Sequence 3473, Ap
c	43	14.8	82.2	3359	4	US-09-023-655-1229	Sequence 1229, Ap
c	44	14.8	82.2	4167	4	US-09-252-991A-3666	Sequence 3666, Ap
	45	14.8	82.2	5859	4	US-09-902-540-823	Sequence 823, App

ALIGNMENTS

RESULT 1
US-09-270-767-1195/c
; Sequence 1195, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1195
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1195

Query Match 91.1%; Score 16.4; DB 4; Length 448;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db         20 TGCGCCGGCGGAGGGGGG 3
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RESULT 2
US-09-270-767-16477/c
; Sequence 16477, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16477
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16477

Query Match 91.1%; Score 16.4; DB 4; Length 448;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TGCGCCGGCGCAGGGGGG 18
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Db         20 TGCGCCGGCGGAGGGGGG 3


RESULT 3
US-09-252-991A-7939
; Sequence 7939, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7939
;   LENGTH: 963
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7939

  Query Match             88.9%;  Score 16;  DB 4;  Length 963;
  Best Local Similarity   100.0%;  Pred. No. 5.7e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCGGCGCAGGGGGG 18
              ||||||||||||||||
Db        906 CGCCGGCGCAGGGGGG 921


RESULT 4
US-09-252-991A-7799
; Sequence 7799, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7799
;   LENGTH: 1050
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7799

  Query Match             88.9%;  Score 16;  DB 4;  Length 1050;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCGGCGCAGGGGGG 18
              ||||||||||||||||
Db       1010 CGCCGGCGCAGGGGGG 1025


RESULT 5
US-10-101-464A-282/c
; Sequence 282, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT:  Nieuwenhuizen, Nicolaas
;  APPLICANT:  Higgins, Colleen M.
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION:  and Their Use in the Modification of Plant Cell Signaling
;  FILE REFERENCE: 11000.1020c2
;  CURRENT APPLICATION NUMBER: US/10/101,464A
;  CURRENT FILING DATE:  2002-03-18
;  PRIOR APPLICATION NUMBER: 09/704,302
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: 09/228,986
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/162,866
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: PCT/US00/00724
;  PRIOR FILING DATE: 2000-01-11
;  NUMBER OF SEQ ID NOS: 989
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 282
;   LENGTH: 900
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-10-101-464A-282

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 900;
  Best Local Similarity   94.1%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||| |||||||||
Db        243 GCGCCGGAGCAGGGGGG 227


RESULT 6
US-09-640-211A-329/c
; Sequence 329, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
;  APPLICANT: Wood, Marion
;  APPLICANT:  Shenk, Michael A.
;  APPLICANT:  McGrath, Annette
;  APPLICANT:  Glenn, Matthew
;  TITLE OF INVENTION: Compositions and Methods for the
;  TITLE OF INVENTION:  Modification of Gene Transcription
;  FILE REFERENCE: 11000.1021C1U
;  CURRENT APPLICATION NUMBER: US/09/640,211A
;  CURRENT FILING DATE:  2000-08-16
;  NUMBER OF SEQ ID NOS: 2368
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 329
;   LENGTH: 1008
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-09-640-211A-329

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 1008;
  Best Local Similarity   94.1%;  Pred. No. 9.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||||| |||||||
Db        236 GCGCCGGCGGAGGGGGG 220


RESULT 7
US-10-101-464A-859/c
; Sequence 859, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT:  Nieuwenhuizen, Nicolaas
;  APPLICANT:  Higgins, Colleen M.
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION:  and Their Use in the Modification of Plant Cell Signaling
;  FILE REFERENCE: 11000.1020c2
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;  CURRENT APPLICATION NUMBER: US/10/101,464A
;  CURRENT FILING DATE:  2002-03-18
;  PRIOR APPLICATION NUMBER: 09/704,302
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: 09/228,986
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/162,866
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: PCT/US00/00724
;  PRIOR FILING DATE: 2000-01-11
;  NUMBER OF SEQ ID NOS: 989
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 859
;   LENGTH: 2478
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-10-101-464A-859

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 2478;
  Best Local Similarity   94.1%;  Pred. No. 8.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||| |||||||||
Db        243 GCGCCGGAGCAGGGGGG 227


RESULT 8
US-09-949-016-15514
; Sequence 15514, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15514
;   LENGTH: 9499
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15514

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 9499;
  Best Local Similarity   94.1%;  Pred. No. 7.6e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||||||||| |||
Db       8381 GCGCCGGCGCAGGAGGG 8397


RESULT 9
US-09-600-319-3/c
; Sequence 3, Application US/09600319
; Patent No. 6780610
; GENERAL INFORMATION:
;  APPLICANT: Owens, Gary
;  APPLICANT:  Madsen, Cort
;  TITLE OF INVENTION: Identification of a Smooth Muscle Cell (SMC) Specific Smooth Musc
;  TITLE OF INVENTION:  Myosin Heavy Chain (SM-MHC) Promoter/Enhancer
;  FILE REFERENCE: 00241-03
;  CURRENT APPLICATION NUMBER: US/09/600,319
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: PCT/US99/01038
;  PRIOR FILING DATE: 1999-01-15
;  PRIOR APPLICATION NUMBER: 60/071,300
;  PRIOR FILING DATE: 1998-01-16
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 16011
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-09-600-319-3

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 16011;
  Best Local Similarity   94.1%;  Pred. No. 7.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              |||| |||||||||||||
Db       4069 GCGCAGGCGCAGGGGGG 4053


RESULT 10
US-09-902-540-1210
; Sequence 1210, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1210
;   LENGTH: 26289
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-1210

  Query Match             85.6%;  Score 15.4;  DB 4;  Length 26289;
  Best Local Similarity   94.1%;  Pred. No. 6.7e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GCGCCGGCGCAGGGGGG 18
              ||||||| |||||||||
Db       1619 GCGCCGGGGCAGGGGGG 1635


RESULT 11
US-09-827-688-8/c
; Sequence 8, Application US/09827688
; Patent No. 6821955
; GENERAL INFORMATION:
;  APPLICANT: ORSON, FRANK
;  APPLICANT:  KINSEY, BERMA
;  APPLICANT:  BHOGAL, BALBIR
;  TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: P01949US1/10004014
;  CURRENT APPLICATION NUMBER: US/09/827,688
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: 60/195,680
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 154746
;   TYPE: DNA
;   ORGANISM: HERPESVIRUS 2
```

US-09-827-688-8

Query Match 85.6%; Score 15.4; DB 4; Length 154746;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 GCGCCGGCGCAGGGGGG 18
              |||| ||||||||||||
Db      68660 GCGCTGGCGCAGGGGGG 68644
```

RESULT 12
US-09-902-540-6323
; Sequence 6323, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6323
; LENGTH: 1771
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6323

Query Match 83.3%; Score 15; DB 4; Length 1771;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GCGCCGGCGCAGGGG 16
              |||||||||||||||
Db         88 GCGCCGGCGCAGGGG 102
```

RESULT 13
US-09-902-540-392
; Sequence 392, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 392
; LENGTH: 2178
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-392

Query Match 83.3%; Score 15; DB 4; Length 2178;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GCGCCGGCGCAGGGG 16
              |||||||||||||||
Db        495 GCGCCGGCGCAGGGG 509
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RESULT 14
US-09-382-552-59
; Sequence 59, Application US/09382552
; Patent No. 6673909
; GENERAL INFORMATION:
; APPLICANT: Brown, Jr., Robert H.
; APPLICANT: Liu, Jing
; APPLICANT: Aoki, Masashi
; APPLICANT: Ho, Meng
; APPLICANT: Matsuda-Asada, Chie
; TITLE OF INVENTION: DYSFERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB
; TITLE OF INVENTION: GIRDLE MUSCULAR DYSTROPHY
; FILE REFERENCE: 00786/399002
; CURRENT APPLICATION NUMBER: US/09/382,552
; CURRENT FILING DATE: 1999-08-25
; EARLIER APPLICATION NUMBER: US 60/097,927
; EARLIER FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-382-552-59

Query Match 82.2%; Score 14.8; DB 4; Length 246;
Best Local Similarity 88.9%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||| ||||||| |||
Db        163 TGCGCCTGCGCAGGAGGG 180
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RESULT 15
US-09-252-991A-3760
; Sequence 3760, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3760
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3760

Query Match 82.2%; Score 14.8; DB 4; Length 426;
Best Local Similarity 88.9%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 TGCGCCGGCGCAGGGGGG 18
              |||||||||||||| || |
Db        124 TGCGCCGGCGCAGCGGCG 141
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Title: US-10-068-160A-31
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Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	6	AX194439	AX194439 Sequence
2	20	100.0	20	6	AX194441	AX194441 Sequence
3	20	100.0	20	6	AX465389	AX465389 Sequence
4	20	100.0	20	6	AX465391	AX465391 Sequence
5	18.4	92.0	20	6	AX194440	AX194440 Sequence
6	18.4	92.0	20	6	AX194481	AX194481 Sequence
7	18.4	92.0	20	6	AX194482	AX194482 Sequence
8	18.4	92.0	20	6	AX194500	AX194500 Sequence
9	18.4	92.0	20	6	AX352202	AX352202 Sequence
10	18.4	92.0	20	6	AX352213	AX352213 Sequence
11	18.4	92.0	20	6	AX352246	AX352246 Sequence
12	18.4	92.0	20	6	AX465390	AX465390 Sequence
13	18.4	92.0	20	6	AX465431	AX465431 Sequence
14	18.4	92.0	20	6	AX465432	AX465432 Sequence
15	18.4	92.0	28	6	AX352223	AX352223 Sequence
16	18.4	92.0	28	6	AX352235	AX352235 Sequence
17	17.4	87.0	19	6	AX194483	AX194483 Sequence
18	17.4	87.0	19	6	AX194488	AX194488 Sequence
19	17.4	87.0	19	6	AX465433	AX465433 Sequence
20	17.4	87.0	19	6	AX465438	AX465438 Sequence
c 21	17.4	87.0	60761	2	AC102704	AC102704 Mus muscu
c 22	17.4	87.0	110000	1	BX571965_25	Continuation (26 o
c 23	17.4	87.0	110000	1	CP000010_15	Continuation (16 o
c 24	17.4	87.0	306650	1	AP005221	AP005221 Corynebac
25	17	85.0	276	11	BV137310	BV137310 PZA00073
26	17	85.0	283	11	BV137300	BV137300 PZA00073
27	17	85.0	317	11	BV137302	BV137302 PZA00073
28	17	85.0	320	11	BV137299	BV137299 PZA00073
29	17	85.0	342	11	BV137315	BV137315 PZA00073
30	17	85.0	343	11	BV137311	BV137311 PZA00073
31	17	85.0	344	11	BV137317	BV137317 PZA00073
32	17	85.0	348	11	BV137318	BV137318 PZA00073
33	17	85.0	349	11	BV137308	BV137308 PZA00073
34	17	85.0	352	11	BV137304	BV137304 PZA00073
35	17	85.0	352	11	BV137312	BV137312 PZA00073
36	17	85.0	354	11	BV137301	BV137301 PZA00073
37	17	85.0	354	11	BV137303	BV137303 PZA00073
38	17	85.0	354	11	BV137306	BV137306 PZA00073
39	17	85.0	354	11	BV137314	BV137314 PZA00073
40	17	85.0	359	11	BV137309	BV137309 PZA00073
41	17	85.0	360	11	BV137316	BV137316 PZA00073
42	17	85.0	363	11	BV137305	BV137305 PZA00073
43	17	85.0	363	11	BV137307	BV137307 PZA00073
44	17	85.0	363	11	BV137313	BV137313 PZA00073
45	16.8	84.0	20	6	AX194432	AX194432 Sequence

ALIGNMENTS

RESULT 1
AX194439
LOCUS AX194439 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 39 from Patent WO0151500.
ACCESSION AX194439
VERSION AX194439.1 GI:15385095
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 39 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 2
AX194441
LOCUS AX194441 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 41 from Patent WO0151500.
ACCESSION AX194441
VERSION AX194441.1 GI:15385097
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 41 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 3
AX465389
LOCUS       AX465389                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 57 from Patent WO0211761.
ACCESSION   AX465389
VERSION     AX465389.1  GI:21899752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 57 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 4
AX465391
LOCUS       AX465391                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 59 from Patent WO0211761.
ACCESSION   AX465391
VERSION     AX465391.1  GI:21899754
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 59 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 5
AX194440
LOCUS       AX194440                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 40 from Patent WO0151500.
ACCESSION   AX194440
VERSION     AX194440.1  GI:15385096
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 40 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 6
AX194481
LOCUS       AX194481                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 81 from Patent WO0151500.
ACCESSION   AX194481
VERSION     AX194481.1  GI:15385137
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 81 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| ||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 7
AX194482
LOCUS       AX194482                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 82 from Patent WO0151500.
ACCESSION   AX194482
VERSION     AX194482.1  GI:15385138
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 82 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| ||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 8
AX194500
LOCUS       AX194500                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 100 from Patent WO0151500.
ACCESSION   AX194500
VERSION     AX194500.1  GI:15385156
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Klinman,D., Ishii,K. and Verthelyi,D.
  TITLE     Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL   Patent: WO 0151500-A 100 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic DNA"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 9
AX352202
LOCUS       AX352202                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 498 from Patent WO0193902.
ACCESSION   AX352202
VERSION     AX352202.1  GI:18617485
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 498 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 10
AX352213
LOCUS       AX352213                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 509 from Patent WO0193902.
ACCESSION   AX352213
VERSION     AX352213.1  GI:18617496
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 509 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match            92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity  95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 11
AX352246
LOCUS       AX352246                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 542 from Patent WO0193902.
ACCESSION   AX352246
VERSION     AX352246.1  GI:18617529
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
```

```
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 542 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 12
AX465390
LOCUS       AX465390                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 58 from Patent WO0211761.
ACCESSION   AX465390
VERSION     AX465390.1  GI:21899753
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 58 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 13
AX465431
LOCUS       AX465431                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 99 from Patent WO0211761.
ACCESSION   AX465431
VERSION     AX465431.1  GI:21899794
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 99 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 14
AX465432
LOCUS       AX465432                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 100 from Patent WO0211761.
ACCESSION   AX465432
VERSION     AX465432.1  GI:21899795
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Prince,G. and Klinman,D.M.
  TITLE     Vaccine against RSV
  JOURNAL   Patent: WO 0211761-A 100 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 7.1e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 15
AX352223
LOCUS       AX352223                  28 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 519 from Patent WO0193902.
ACCESSION   AX352223
VERSION     AX352223.1  GI:18617506
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 519 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic HDR"
ORIGIN

  Query Match             92.0%;  Score 18.4;  DB 6;  Length 28;
  Best Local Similarity   95.0%;  Pred. No. 6.8e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20
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Job time : 792.476 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 203.919 Seconds
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Title: US-10-068-160A-31
Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	4	AAC80619	Aac80619 Immunogen
2	20	100.0	20	4	AAC80621	Aac80621 Immunogen
3	20	100.0	20	4	AAS09591	Aas09591 Immunorea
4	20	100.0	20	4	AAS09589	Aas09589 Immunorea
5	20	100.0	20	6	ABK46469	Abk46469 Immunosti
6	20	100.0	20	6	ABK46467	Abk46467 Immunosti
7	20	100.0	20	8	ACC48315	Acc48315 CpG oligo
8	20	100.0	20	9	ACC83120	Acc83120 D class C
9	20	100.0	20	10	ADD01055	Add01055 CpG D oli
10	18.4	92.0	20	4	AAC80662	Aac80662 Immunogen
11	18.4	92.0	20	4	AAC80661	Aac80661 Immunogen
12	18.4	92.0	20	4	AAC80620	Aac80620 Immunogen
13	18.4	92.0	20	4	AAS09650	Aas09650 Immunorea
14	18.4	92.0	20	4	AAS09631	Aas09631 Immunorea
15	18.4	92.0	20	4	AAS09590	Aas09590 Immunorea
16	18.4	92.0	20	4	AAS09632	Aas09632 Immunorea
17	18.4	92.0	20	6	ABL35616	Abl35616 Immunosti
18	18.4	92.0	20	6	ABL35572	Abl35572 Immunosti
19	18.4	92.0	20	6	ABL35583	Abl35583 Immunosti
20	18.4	92.0	20	6	ABK46510	Abk46510 Immunosti
21	18.4	92.0	20	6	ABK46468	Abk46468 Immunosti
22	18.4	92.0	20	6	ABK46509	Abk46509 Immunosti
23	18.4	92.0	20	8	ACC48298	Acc48298 CpG oligo
24	18.4	92.0	20	8	ACC48312	Acc48312 CpG oligo
25	18.4	92.0	20	8	ACC48314	Acc48314 CpG oligo
26	18.4	92.0	20	8	ACC48319	Acc48319 CpG oligo
27	18.4	92.0	20	9	ACC83119	Acc83119 D class C
28	18.4	92.0	20	9	ACC83117	Acc83117 D class C
29	18.4	92.0	20	9	ACC83124	Acc83124 D class C
30	18.4	92.0	20	10	ADD01050	Add01050 CpG D oli
31	18.4	92.0	20	10	ADD01057	Add01057 CpG D oli
32	18.4	92.0	20	12	ADN96882	Adn96882 Immunosti
33	18.4	92.0	28	6	ABL35605	Abl35605 Immunosti
34	18.4	92.0	28	6	ABL35593	Abl35593 Immunosti
35	18	90.0	20	8	ACC48301	Acc48301 CpG oligo
36	18	90.0	20	12	ADN96869	Adn96869 Immunosti
37	17.4	87.0	19	4	AAC80663	Aac80663 Immunogen
38	17.4	87.0	19	4	AAC80668	Aac80668 Immunogen
39	17.4	87.0	19	4	AAS09633	Aas09633 Immunorea
40	17.4	87.0	19	4	AAS09638	Aas09638 Immunorea
41	17.4	87.0	19	6	ABK46516	Abk46516 Immunosti
42	17.4	87.0	19	6	ABK46511	Abk46511 Immunosti
43	16.8	84.0	20	4	AAC80652	Aac80652 Immunogen
44	16.8	84.0	20	4	AAC80614	Aac80614 Immunogen
45	16.8	84.0	20	4	AAC80612	Aac80612 Immunogen

ALIGNMENTS

RESULT 1
AAC80619
ID AAC80619 standard; DNA; 20 BP.
XX
AC AAC80619;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:39.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX

PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 2
AAC80621
ID AAC80621 standard; DNA; 20 BP.
XX
AC AAC80621;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:41.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 3

AAS09591
ID AAS09591 standard; DNA; 20 BP.
XX
AC AAS09591;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #41.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 34; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
|||||||||||||||||||| |
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 4
AAS09589
ID AAS09589 standard; DNA; 20 BP.
XX
AC AAS09589;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #39.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 33; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 20;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 5
ABK46469
ID   ABK46469 standard; DNA; 20 BP.
XX
AC   ABK46469;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Immunostimulatory unmethylated CpG oligodideoxynucleotide #59.
XX
KW   unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW   Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW   viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW   bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS   Synthetic.
XX
PN   WO200211761-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US041633.
XX
PR   10-AUG-2000; 2000US-0224011P.
PR   01-SEP-2000; 2000US-0229307P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Mond JJ,  Prince G,  Klinman DM;
XX
DR   WPI; 2002-227118/28.
XX
PT   Vaccine for immunizing patient against respiratory syncytial virus, has
PT   epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT   linked by phosphate bond-oligodideoxynucleotides.
XX
PS   Claim 4; Page 8; 30pp; English.
XX
CC   The invention describes a vaccine comprising one or more epitopes of a
CC   Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC   guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC   vaccine is useful for vaccinating a patient especially against viruses of
CC   the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC   primary cause of viral bronchiolitis and pneumonia in infants and
CC   children, and infectious pulmonary disease in infants. RSV has been
CC   particularly implicated in death of infants that are premature, have
CC   bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC   represents an oligodideoxynucleotide that can be used in the creation of
CC   the vaccine
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 6
ABK46467
ID   ABK46467 standard; DNA; 20 BP.
XX
AC   ABK46467;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Immunostimulatory unmethylated CpG oligodideoxynucleotide #57.
XX
KW   unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW   Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW   viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW   bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS   Synthetic.
XX
PN   WO200211761-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US041633.
XX
PR   10-AUG-2000; 2000US-0224011P.
PR   01-SEP-2000; 2000US-0229307P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Mond JJ,  Prince G,  Klinman DM;
XX
DR   WPI; 2002-227118/28.
XX
PT   Vaccine for immunizing patient against respiratory syncytial virus, has
PT   epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT   linked by phosphate bond-oligodideoxynucleotides.
XX
PS   Claim 4; Page 8; 30pp; English.
XX
CC   The invention describes a vaccine comprising one or more epitopes of a
CC   Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC   guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC   vaccine is useful for vaccinating a patient especially against viruses of
CC   the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC   primary cause of viral bronchiolitis and pneumonia in infants and
CC   children, and infectious pulmonary disease in infants. RSV has been
CC   particularly implicated in death of infants that are premature, have
CC   bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC   represents an oligodideoxynucleotide that can be used in the creation of
CC   the vaccine
XX
SQ   Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 7
ACC48315
ID   ACC48315 standard; DNA; 20 BP.
XX
AC   ACC48315;
XX
DT   11-AUG-2003  (first entry)
XX
DE   CpG oligodeoxynucleotide DV32.
XX
KW   CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW   cytostatic; immunostimulant; gene therapy; ss.
XX
OS   Synthetic.
XX
```

PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
PT for activating the immune system to treat diseases such as cancer,
PT comprises contacting a dendritic cell precursor with a D type
PT oligodeoxynucleotide.
XX
PS Disclosure; Fig 8; 69pp; English.
XX
CC The present sequence is that of CpG oligodeoxynucleotide DV32 of the
CC invention. A claimed method for generating dendritic cells involves
CC contacting a dendritic cell precursor, especially a monocyte, with a D
CC type oligodeoxynucleotide (see ACC48294) containing a central
CC unmethylated CpG motif. The method is useful for generating mature
CC dendritic cells and enhancing T cell responses, thus enhancing antigen
CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
CC for augmenting an immune response to an infectious agent or to a vaccine,
CC and as vaccines to prevent future infection or to activate the immune
CC system to treat diseases such as cancer. Mature dendritic cells may also
CC be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 8
ACC83120
ID ACC83120 standard; DNA; 20 BP.
XX
AC ACC83120;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV32.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.
XX
OS Unidentified.
XX
PN WO2003040308-A2.
XX
PD 15-MAY-2003.
XX
PF 29-JUL-2002; 2002WO-US024235.
XX
PR 27-JUL-2001; 2001US-0308283P.
PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10C; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc); allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 9
ADD01055
ID ADD01055 standard; DNA; 20 BP.
XX
AC ADD01055;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG D oligonucleotide SEQ ID NO:19.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerary; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
PN WO2003054161-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Zheng M, Rouse BT;
XX

DR WPI; 2003-559138/52.
XX
PT Inducing the production of vascular endothelial growth factor by a cell,
PT useful for inducing angiogenesis, comprises contacting the cell with a
PT CpG oligodeoxynucleotide.
XX
PS Example 7; SEQ ID NO 19; 37pp; English.
XX
CC The present invention describes a method for inducing the production of
CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC the cell with a CpG oligonucleotide and therefore inducing the production
CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC tissue, comprising introducing a CpG oligonucleotide into an area of the
CC tissue where the formation of new blood vessels is desired, and so
CC inducing neovascularisation in the area of the tissue; (2) promoting
CC angiogenesis in an area of the subject where angiogenesis is desired,
CC comprising introducing a CpG oligonucleotide to the area, and so
CC promoting angiogenesis in the subject; and (3) screening for an agent
CC that inhibits neovascularisation, comprising administering a CpG
CC oligonucleotide to a non-human mammal and administering the agent to the
CC mammal, where inhibition of angiogenesis in the animal indicates that the
CC agent is effective in inhibiting neovascularisation. The CpG
CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC activities, and can be used in gene therapy. The method and the CpG
CC oligonucleotides can be used in inducing angiogenesis or
CC neovascularisation, such as in subjects with a skin graft, subjects who
CC exhibit male pattern baldness, or subjects who have a wound or who have
CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a CpG oligonucleotide which is used in the exemplification of
CC the present invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 10
AAC80662
ID AAC80662 standard; DNA; 20 BP.
XX
AC AAC80662;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 36; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
|||||||||| |||||||||
Db 1 GGTGCGTCGATGCAGGGGGG 20

RESULT 11
AAC80661
ID AAC80661 standard; DNA; 20 BP.
XX
AC AAC80661;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 36; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||| |||||||||
Db 1 GGTGCGTCGATGCAGGGGGG 20

RESULT 12
AAC80620
ID AAC80620 standard; DNA; 20 BP.
XX
AC AAC80620;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 30; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or

CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||| |||||||||
Db 1 GGTGCGTCGATGCAGGGGGG 20

RESULT 13
AAS09650
ID AAS09650 standard; DNA; 20 BP.
XX
AC AAS09650;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #100.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 43; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||| ||||||||||||||
Db 1 GGTGCATCGACGCAGGGGGG 20

RESULT 14
AAS09631
ID AAS09631 standard; DNA; 20 BP.
XX
AC AAS09631;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #81.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.

XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 40; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||.|||||||||
Db 1 GGTGCGTCGATGCAGGGGGG 20

RESULT 15
AAS09590
ID AAS09590 standard; DNA; 20 BP.
XX
AC AAS09590;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #40.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 33; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||.|||||||||
Db 1 GGTGCGTCGATGCAGGGGGG 20

Search completed: April 29, 2005, 06:26:04
Job time : 203.919 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1875.14 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-31
Perfect score: 20
Sequence: 1 ggtgcgtcgacgcaggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.4	87.0	241	1	AA807153	oc36d11.s
	2	17.4	87.0	349	5	BU038662	BU038662 DH02G09 H
c	3	17.4	87.0	467	8	AQ221882	AQ221882 HS_2240_A
	4	17	85.0	443	2	BE453868	BE453868 946047E07
	5	17	85.0	469	2	BE510146	BE510146 946047E07
	6	17	85.0	469	8	BZ583033	BZ583033 3590_1_49
	7	17	85.0	481	3	AY106226	AY106226 Zea mays
c	8	17	85.0	488	9	CG305844	CG305844 OG0BX58TV
	9	17	85.0	502	4	BM428951	BM428951 952026C01
	10	17	85.0	541	9	CG305830	CG305830 OG0BX58TH
	11	17	85.0	573	5	BU499653	BU499653 946178A11
	12	17	85.0	600	5	BU049816	BU049816 1111015B0
	13	17	85.0	795	9	CG303497	CG303497 OG1AI84TH
	14	17	85.0	970	9	CG299311	CG299311 OG2BJ70TV
	15	17	85.0	1032	9	CL987494	CL987494 ZMMBHe000
	16	16.8	84.0	249	9	AG063742	AG063742 Pan trogl
	17	16.8	84.0	257	1	AV268287	AV268287 AV268287
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c	19	16.8	84.0	382	4	BJ492497	BJ492497 BJ492497
c	20	16.8	84.0	435	6	CA724998	CA724998 wds3f.pk0
c	21	16.8	84.0	448	6	CA692841	CA692841 wlm96.pk0
c	22	16.8	84.0	456	6	CA721629	CA721629 wdk9n1.pk
	23	16.8	84.0	463	6	CA284955	CA284955 SCEPSD107
	24	16.8	84.0	488	6	CA180503	CA180503 SCCCST300
c	25	16.8	84.0	501	6	CA659573	CA659573 wlm1.pk00
c	26	16.8	84.0	505	5	BQ606855	BQ606855 BRY_2730
	27	16.8	84.0	513	9	CL965042	CL965042 OsIFCC011
c	28	16.8	84.0	539	2	BE498422	BE498422 WHE0967_H
	29	16.8	84.0	543	6	CA162989	CA162989 SCRLRZ304
c	30	16.8	84.0	554	4	BG904417	BG904417 TaLr1132A
	31	16.8	84.0	561	6	CA138317	CA138317 SCEQRT202
c	32	16.8	84.0	576	6	CA613400	CA613400 wr1.pk014
c	33	16.8	84.0	581	9	CL562112	CL562112 OB__Ba002
	34	16.8	84.0	584	6	CA095014	CA095014 SCCCCL401
c	35	16.8	84.0	584	6	CA226594	CA226594 SCRLFL300
	36	16.8	84.0	586	6	CA074434	CA074434 SCEZAM108
c	37	16.8	84.0	586	8	AQ288864	AQ288864 nbxb0033F
c	38	16.8	84.0	592	4	BJ209668	BJ209668 BJ209668
	39	16.8	84.0	594	6	CA131005	CA131005 SCBFRT106
	40	16.8	84.0	596	6	CA196543	CA196543 SCBFAD109
c	41	16.8	84.0	599	6	CA154602	CA154602 SCCCRZ300
c	42	16.8	84.0	600	6	CA728680	CA728680 wdi1c.pk0
c	43	16.8	84.0	601	6	CD862102	CD862102 AZO1.102G
c	44	16.8	84.0	605	6	CA147091	CA147091 SCCCRZ100
	45	16.8	84.0	606	6	CA145644	CA145644 SCSGRT206

ALIGNMENTS

RESULT 1
AA807153
LOCUS AA807153 241 bp mRNA linear EST 07-APR-1998
DEFINITION oc36d11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351797 3' similar to gb:X03910 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN UP2 (HUMAN);, mRNA sequence.
ACCESSION AA807153
VERSION AA807153.1 GI:2876729
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 241)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1579 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1351797"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

```
  Query Match             87.0%;  Score 17.4;  DB 1;  Length 241;
  Best Local Similarity   94.7%;  Pred. No. 9.6e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGG 19
              |||||||||||  |||||||
Db         47 GGTGCGTCGACACAGGGGG 65
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RESULT 2
BU038662
LOCUS BU038662 349 bp mRNA linear EST 23-AUG-2002
DEFINITION DH02G09 Helicoverpa armigera larval midgut cDNA library Helicoverpa armigera cDNA 5', mRNA sequence.
ACCESSION BU038662
VERSION BU038662.1 GI:22474186
KEYWORDS EST.
SOURCE Helicoverpa armigera (cotton bollworm)
ORGANISM Helicoverpa armigera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
REFERENCE 1 (bases 1 to 349)
AUTHORS Grubor,V., Kuczek,E., Wilson,P. and Heckel,D.G.
TITLE Construction and analysis of a cDNA library from larval midguts of cotton bollworm Helicoverpa armigera
JOURNAL Unpublished (2002)
COMMENT Contact: Vladimir Grubor
CESAR--Centre for Environmental Stress and Adaptation Research
Department of Genetics, The University of Melbourne
Parkville, Victoria, 3010, Australia
Tel: +61 3 8344 6246
Fax: +61 3 8344 5139
Email: vgrubor@pgrad.unimelb.edu.au
Seq primer: T3 Forward.
FEATURES Location/Qualifiers
source 1. .349
/organism="Helicoverpa armigera"
/mol_type="mRNA"
/strain="AN02"
/db_xref="taxon:29058"
/tissue_type="Midgut"
/dev_stage="Fifth instar larvae"
/lab_host="XL1-Blue MRF'"
/clone_lib="Helicoverpa armigera larval midgut cDNA library"
/note="Vector: pBluescript II SK(-); Total RNA was prepared from midguts of mid-fifth instar larvae of Helicoverpa armigera using the RNAgents kit (Promega). PolyA mRNA was obtained using the Dynabeads mRNA purification kit (Dynal). First-strand cDNA was made by oligo dT-priming with 5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTT-3'. Following second-strand cDNA synthesis, size-selected products >600 bp were ligated to 5' linkers 5'-AATTCGGCACGAGG-3' and 5'-CCTCGTGCCG-3', directionally cloned into Lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites, and packaged using Gigapack III Gold Packaging Extracts. The library was amplified, and plasmids were mass-excised using ExAssist helper phage (Stratagene) and propagated in XL1-Blue MRF' cells. Single-pass 5' end sequencing was performed using the T3 primer. Library construction supported by CESAR, a Special Research Centre of the Australian Research Council. Sequencing supported by the Director's Discretionary Fund of the Australian Genome Research Facility."

ORIGIN

```
  Query Match             87.0%;  Score 17.4;  DB 5;  Length 349;
  Best Local Similarity   94.7%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGG 19
              |||||| ||||||||||||
Db        113 GGTGCGCCGACGCAGGGGG 131
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RESULT 3
AQ221882/c
LOCUS AQ221882 467 bp DNA linear GSS 19-SEP-1998
DEFINITION HS_2240_A1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2240 Col=3 Row=O, genomic survey sequence.
ACCESSION AQ221882
VERSION AQ221882.1 GI:3635495
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 467)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2240 row: O column: 3
Class: BAC ends
High quality sequence stop: 467.
FEATURES Location/Qualifiers
source 1. .467
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2240 Col=3 Row=O"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

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  Query Match             87.0%;  Score 17.4;  DB 8;  Length 467;
  Best Local Similarity   94.7%;  Pred. No. 8.9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGG 19
              ||||||| ||||||||||||
Db        190 GGTGCGTGGACGCAGGGGG 172
```

RESULT 4
BE453868
LOCUS BE453868 443 bp mRNA linear EST 26-JUL-2000
DEFINITION 946047E07.y1 946 - tassel primordium prepared by Schmidt lab Zea

```
          mays cDNA, mRNA sequence.
ACCESSION   BE453868
VERSION     BE453868.1  GI:9461714
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946047  row: E  column: 07.
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
ORIGIN

  Query Match             85.0%;  Score 17;  DB 2;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        128 GTGCGTCGACGCAGGGG 144


RESULT 5
BE510146
LOCUS       BE510146                469 bp    mRNA    linear   EST 07-AUG-2000
DEFINITION  946047E07.y2 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BE510146
VERSION     BE510146.1  GI:9731394
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946047  row: E  column: 07.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
ORIGIN

  Query Match             85.0%;  Score 17;  DB 2;  Length 469;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        118 GTGCGTCGACGCAGGGG 134


RESULT 6
BZ583033
LOCUS       BZ583033                469 bp    DNA     linear   GSS 17-DEC-2002
DEFINITION  3590_1_49_1_A01.y_1 3590 - RescueMu Grid M Zea mays genomic,
            genomic survey sequence.
ACCESSION   BZ583033
VERSION     BZ583033.1  GI:27218094
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 3590_1_49_1  column: 10
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="3590 - RescueMu Grid M"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
```

site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid M was grown at University of Arizona in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 85.0%; Score 17; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GTGCGTCGACGCAGGGG 18
              ||||||||||||||||||
Db        261 GTGCGTCGACGCAGGGG 277
```

RESULT 7
AY106226
LOCUS AY106226 481 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PCO146698 mRNA sequence.
ACCESSION AY106226
VERSION AY106226.1 GI:21209304
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 481)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 481)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
source 1. .481
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:638670"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 85.0%; Score 17; DB 3; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GTGCGTCGACGCAGGGG 18
              ||||||||||||||||||
Db        259 GTGCGTCGACGCAGGGG 275
```

RESULT 8
CG305844/c
LOCUS CG305844 488 bp DNA linear GSS 25-AUG-2003
DEFINITION OG0BX58TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0683I20, genomic survey sequence.
ACCESSION CG305844
VERSION CG305844.1 GI:34220058
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 488)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OG0BX58TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .488
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMa0683I20"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GTGCGTCGACGCAGGGG 18
              ||||||||||||||||||
Db        214 GTGCGTCGACGCAGGGG 198
```

RESULT 9
BM428951
LOCUS BM428951 502 bp mRNA linear EST 31-JAN-2002
DEFINITION 952026C01.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.
ACCESSION BM428951
VERSION BM428951.1 GI:18450673
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 502)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

```
          Plate: 952026  row: C  column: 01.
FEATURES             Location/Qualifiers
     source          1. .502
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="BMS (Black Mexican Sweet)"
                     /db_xref="taxon:4577"
                     /tissue_type="suspension culture"
                     /dev_stage="mixed logarithmic and stationary growth
                     phases"
                     /lab_host="DH10B"
                     /clone_lib="952 - BMS tissue from Walbot Lab (reduced
                     rRNA)"
                     /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The
                     library was prepared by George Rudenko using poly (A)
                     selected RNA and Universal Riboclone cDNA Synthesis System
                     (Promega). cDNA was synthesized using both random and
                     oligo(dT) primers in separate reactions and equipped with
                     EcoRI adaptors. Library was size-fractionated on agarose
                     gels (for insert size >400bp) and non-directionally cloned
                     into EcoRI-digested pUC19 vector. Blue/white selection on
                     carbenicillin-containing plates was used to recover
                     positive clones."
ORIGIN

  Query Match             85.0%;  Score 17;  DB 4;  Length 502;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        181 GTGCGTCGACGCAGGGG 197


RESULT 10
CG305830
LOCUS       CG305830                541 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG0BX58TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0683I20,
            genomic survey sequence.
ACCESSION   CG305830
VERSION     CG305830.1  GI:34220044
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG0BX58TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .541
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0683I20"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 541;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        275 GTGCGTCGACGCAGGGG 291


RESULT 11
BU499653
LOCUS       BU499653                573 bp    mRNA    linear   EST 12-SEP-2002
DEFINITION  946178A11.y1 946 - tassel primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION   BU499653
VERSION     BU499653.1  GI:22819563
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946178  row: A  column: 11.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="OH43"
                     /db_xref="taxon:4577"
                     /tissue_type="tassels"
                     /dev_stage="just after the transition from vegetative to
                     inflorescence development"
                     /lab_host="XLOLR"
                     /clone_lib="946 - tassel primordium prepared by Schmidt
                     lab"
                     /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
                     Site_2: XhoI; George Chuck dissected immature tassels
                     between 1mm and 3mm.  Sharon  Stanfield prepared the cDNA
                     library in HybriZAP.  Sample insert size  range was 350 bp
                     to 3 Kb with a 1 Kb average."
ORIGIN

  Query Match             85.0%;  Score 17;  DB 5;  Length 573;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        141 GTGCGTCGACGCAGGGG 157


RESULT 12
BU049816
LOCUS       BU049816                600 bp    mRNA    linear   EST 26-AUG-2002
DEFINITION  1111015B03.y1 1111 - Unigene III from Maize Genome Project Zea mays
            cDNA, mRNA sequence.
ACCESSION   BU049816
VERSION     BU049816.1  GI:22489893
KEYWORDS    EST.
SOURCE      Zea mays
```

```
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Walbot,V.
  TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1111015  row: B  column: 03.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="dbEST:952026C01.y1"
                     /db_xref="taxon:4577"
                     /clone_lib="1111 - Unigene III from Maize Genome Project"
                     /note="This library represents the unique genes found in
                     the third round of EST sequencing at Stanford University
                     for the maize genome project. Sequences are present from
                     library 952. Contigs were assembled using ZmDBAssembler
                     and 2 representatives from each contig were selected for
                     the Unigene set. All singlets were also selected."
ORIGIN

  Query Match             85.0%;  Score 17;  DB 5;  Length 600;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        175 GTGCGTCGACGCAGGGG 191


RESULT 13
CG303497
LOCUS       CG303497                 795 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG1AI84TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0717M23,
            genomic survey sequence.
ACCESSION   CG303497
VERSION     CG303497.1  GI:34217711
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG1AI84TV
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0717M23"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 795;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
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Db        336 GTGCGTCGACGCAGGGG 352


RESULT 14
CG299311
LOCUS       CG299311                 970 bp    DNA     linear   GSS 25-AUG-2003
DEFINITION  OG2BJ70TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0752L20,
            genomic survey sequence.
ACCESSION   CG299311
VERSION     CG299311.1  GI:34213525
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Other_GSSs: OG2BJ70TH
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBMa0752L20"
                     /clone_lib="ZM_0.7_1.5_KB"
                     /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 970;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
              |||||||||||||||||
Db        419 GTGCGTCGACGCAGGGG 435


RESULT 15
CL987494
LOCUS       CL987494                1032 bp    DNA     linear   GSS 23-SEP-2004
DEFINITION  ZMMBHe0004d07.r ZMMBHe Zea mays genomic clone ZMMBHe0004d07 3',
            genomic survey sequence.
ACCESSION   CL987494
VERSION     CL987494.1  GI:52555572
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KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1032)
  AUTHORS   Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and
            Bennetzen,J.
  TITLE     ZMMBH sequences
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Jeff Bennetzen
            Bennetzen Lab
            The University of Georgia
            Department of Genetics, C426a Life Sciences Building, Athens, GA
            30602, USA
            Tel: 706-542-3698
            Fax: 706-583-0972
            Email: maize@uga.edu
            Plate: 0004  row: d  column: 07
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .1032
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBHe0004d07"
                     /tissue_type="immature ear"
                     /dev_stage="6-8 weeks"
                     /lab_host="DH10B"
                     /clone_lib="ZMMBHe"
                     /note="Vector: TOPOpcr4; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN

  Query Match             85.0%;  Score 17;  DB 9;  Length 1032;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGG 18
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Db         70 GTGCGTCGACGCAGGGG 86


Search completed: April 29, 2005, 11:55:26
Job time : 1877.14 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 58.5135 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-31
Perfect score: 20
Sequence: 1 ggtgcgtcgacgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		16.8	84.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
2		16.8	84.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
3	c	15.8	79.0	1074	4	US-09-252-991A-5833	Sequence 5833, Ap
4		15.8	79.0	1554	4	US-09-252-991A-5777	Sequence 5777, Ap
5	c	15.8	79.0	9818	4	US-09-902-540-987	Sequence 987, App
6	c	15.2	76.0	157	4	US-09-513-999C-22184	Sequence 22184, A
7		15.2	76.0	531	3	US-08-840-551-3	Sequence 3, Appli
8	c	15.2	76.0	1161	4	US-09-489-039A-6181	Sequence 6181, Ap
9	c	15.2	76.0	1999	4	US-09-472-087-54	Sequence 54, Appl
10	c	15.2	76.0	2029	2	US-07-916-098A-43	Sequence 43, Appl
11	c	15.2	76.0	2249	4	US-09-627-896B-23	Sequence 23, Appl
12	c	15.2	76.0	2399	2	US-08-070-116A-1	Sequence 1, Appli
13	c	15.2	76.0	2399	4	US-08-557-050-1	Sequence 1, Appli
14	c	15.2	76.0	2482	3	US-08-477-460B-3	Sequence 3, Appli
15	c	15.2	76.0	2482	3	US-08-379-516-3	Sequence 3, Appli
16	c	15.2	76.0	2482	3	US-09-329-916-3	Sequence 3, Appli
17	c	15.2	76.0	2482	3	US-08-485-372A-3	Sequence 3, Appli
18	c	15.2	76.0	2482	3	US-09-409-006A-3	Sequence 3, Appli
19	c	15.2	76.0	2482	3	US-08-484-681-3	Sequence 3, Appli
20	c	15.2	76.0	2482	4	US-09-766-995-3	Sequence 3, Appli
21	c	15.2	76.0	2482	5	PCT-US93-07422-3	Sequence 3, Appli
22	c	15.2	76.0	2560	2	US-07-916-098A-44	Sequence 44, Appl
23		15.2	76.0	4649	6	5183745-1	Patent No. 5183745
24		15.2	76.0	4649	6	5183745-1	Patent No. 5183745
25		15.2	76.0	5118	3	US-08-669-785-3	Sequence 3, Appli
26		15.2	76.0	6441	3	US-08-669-785-1	Sequence 1, Appli
27		15.2	76.0	6443	6	5183745-5	Patent No. 5183745
28		15.2	76.0	6443	6	5183745-5	Patent No. 5183745
29	c	15.2	76.0	10785	3	US-08-444-644-27	Sequence 27, Appl
30	c	15.2	76.0	10785	3	US-08-232-246A-27	Sequence 27, Appl
31	c	15.2	76.0	10844	3	US-08-444-644-41	Sequence 41, Appl
32	c	15.2	76.0	10844	3	US-08-232-246A-41	Sequence 41, Appl
33		15.2	76.0	12082	4	US-09-949-016-16487	Sequence 16487, A
34	c	15.2	76.0	36941	4	US-08-311-731A-130	Sequence 130, App
35	c	15.2	76.0	42325	4	US-08-311-731A-131	Sequence 131, App
36	c	15.2	76.0	59853	4	US-09-949-016-13618	Sequence 13618, A
37	c	15.2	76.0	59853	4	US-09-949-016-13619	Sequence 13619, A
38	c	15.2	76.0	59853	4	US-09-949-016-13620	Sequence 13620, A
39	c	15.2	76.0	59853	4	US-09-949-016-13621	Sequence 13621, A
40	c	15.2	76.0	59853	4	US-09-949-016-13622	Sequence 13622, A
41	c	15.2	76.0	59853	4	US-09-949-016-13623	Sequence 13623, A
42	c	15.2	76.0	59853	4	US-09-949-016-13624	Sequence 13624, A
43	c	15.2	76.0	59853	4	US-09-949-016-13625	Sequence 13625, A
44		15.2	76.0	97989	4	US-09-949-016-13208	Sequence 13208, A
45	c	15.2	76.0	118999	4	US-09-791-105B-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 84.0%; Score 16.8; DB 3; Length 4403765;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2

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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             84.0%;  Score 16.8;  DB 3;  Length 4411529;
  Best Local Similarity   90.0%;  Pred. No. 54;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT 3
US-09-252-991A-5833/c
; Sequence 5833, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 5833
;   LENGTH: 1074
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5833

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 1074;
  Best Local Similarity   89.5%;  Pred. No. 2.5e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT 4
US-09-252-991A-5777
; Sequence 5777, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 5777
;   LENGTH: 1554
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5777

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Qy          1 GGTGCGTCGACGCAGGGGG 19
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Db       1368 GGTGCGTCGACGCGTGGGG 1386


RESULT 5
US-09-902-540-987/c
; Sequence 987, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 987
;   LENGTH: 9818
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-987

  Query Match             79.0%;  Score 15.8;  DB 4;  Length 9818;
  Best Local Similarity   89.5%;  Pred. No. 2.2e+02;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 GTGCGTCGACGCAGGGGGG 20
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Db       8556 GTGGGTCGACGCAGAGGGG 8538


RESULT 6
US-09-513-999C-22184/c
; Sequence 22184, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 22184
;   LENGTH: 157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7
;   OTHER INFORMATION: b=c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 8
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 116
;   OTHER INFORMATION: s=g or c
US-09-513-999C-22184

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 157;
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  Best Local Similarity   85.0%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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RESULT 7
US-08-840-551-3
; Sequence 3, Application US/08840551B
; Patent No. 6066449
; GENERAL INFORMATION:
;  APPLICANT: Ditkoff, Beth A., et al.
;  TITLE OF INVENTION: METHOD OF DETECTING METASTATIC THYROID CANCER
;  FILE REFERENCE: 0575/51662/jpw/jkm
;  CURRENT APPLICATION NUMBER: US/08/840,551B
;  CURRENT FILING DATE: 1997-04-15
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 531
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: OTHER NUCLEIC
;   OTHER INFORMATION: ACID
US-08-840-551-3

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 531;
  Best Local Similarity   85.0%;  Pred. No. 4.9e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||  ||  ||||||| ||||
Db        385 GGTGTGTGGACGCAGAGGGG 404


RESULT 8
US-09-489-039A-6181/c
; Sequence 6181, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 6181
;   LENGTH: 1161
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6181

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 1161;
  Best Local Similarity   85.0%;  Pred. No. 4.7e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
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Db        392 GGTGCGTCGGCGCCGGGGCG 373


RESULT 9
US-09-472-087-54/c
; Sequence 54, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 1999
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-54

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 1999;
  Best Local Similarity   85.0%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
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Db        776 GGTGCGTCCAGGCAGGAGGG 757


RESULT 10
US-07-916-098A-43/c
; Sequence 43, Application US/07916098A
; Patent No. 5871732
;  GENERAL INFORMATION:
;    APPLICANT:  BURKLY, LINDA C.
;    APPLICANT:  CHISHOLM, PATRICIA L.
;    APPLICANT:  THOMAS, DAVID W.
;    APPLICANT:  ROSA, MARGARET D.
;    APPLICANT:  ROSA, JOSEPH J.
;    TITLE OF INVENTION:  ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;    TITLE OF INVENTION:  PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
;      STREET:  10 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,098A
;      FILING DATE:  July 24, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 5871732ember 27, 1991
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/618,542
;      FILING DATE:  No. 5871732ember 27, 1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JOHN J. MC DONNELL
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,310-G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;      TELEX:  910/221-5317
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;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2029 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pBAG101 insert"
US-07-916-098A-43

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 2029;
  Best Local Similarity   85.0%;  Pred. No. 4.6e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||| | ||||| |||
Db        581 GGTGCGTCCAGGCAGGAGGG 562


RESULT 11
US-09-627-896B-23/c
; Sequence 23, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILIANO
;  APPLICANT:  CARRENO, BEATRIZ
;  APPLICANT:  CELNIKER, ABBIE CHERYL
;  APPLICANT:  COLLINS, MARY
;  APPLICANT:  GOLDMAN, SAMUEL
;  APPLICANT:  GRAY, GARY S.
;  APPLICANT:  KNIGHT, ANDREA
;  APPLICANT:  O'HARA, DENISE
;  APPLICANT:  RUP, BONITA
;  APPLICANT:  VELDMAN, GEERTRUIDA M.
;  TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;  TITLE OF INVENTION:  OF TREATMENT THEREWITH
;  FILE REFERENCE: 08702.0081-01000
;  CURRENT APPLICATION NUMBER: US/09/627,896B
;  CURRENT FILING DATE:  2000-07-27
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: 3D1 heavy chain
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (12)..(417)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (655)..(948)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1341)..(1376)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1495)..(1821)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1919)..(2238)
US-09-627-896B-23

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 2249;
  Best Local Similarity   85.0%;  Pred. No. 4.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||| | ||||| |||
Db       1018 GGTGCGTCCAGGCAGGAGGG 999


RESULT 12
US-08-070-116A-1/c
; Sequence 1, Application US/08070116A
; Patent No. 5885573
;  GENERAL INFORMATION:
;    APPLICANT:  Zivin, Robert A.
;    APPLICANT:  Jolliffe, Linda K.
;    APPLICANT:  Bluestone, Jeffrey A.
;    TITLE OF INVENTION:  Methods and Materials For Modulation
;    TITLE OF INVENTION:  of the Immuno-suppressive Activity and
;    TITLE OF INVENTION:  Toxicity of Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/070,116A
;      FILING DATE:  01-JUN-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  ARCD:082
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..760
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1151..1186
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1308..1634
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1732..2055
US-08-070-116A-1

  Query Match             76.0%;  Score 15.2;  DB 2;  Length 2399;
  Best Local Similarity   85.0%;  Pred. No. 4.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||| | ||||| |||
Db        831 GGTGCGTCCAGGCAGGAGGG 812


RESULT 13
US-08-557-050-1/c
; Sequence 1, Application US/08557050
; Patent No. 6491916
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;  GENERAL INFORMATION:
;    APPLICANT:  Bluestone, Jeffrey A.
;    APPLICANT:  Zivin, Robert A.
;    APPLICANT:  Jolliffe, Linda K.
;    TITLE OF INVENTION:  METHODS AND MATERIALS FOR MODULATION OF
;    TITLE OF INVENTION:  THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,050
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/06198
;      FILING DATE:  01-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/070,116
;      FILING DATE:  01-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wilson, Mark B.
;      REGISTRATION NUMBER:  37,259
;      REFERENCE/DOCKET NUMBER:  ARCD:208
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  53..760
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1151..1186
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1308..1634
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1732..2052
US-08-557-050-1

  Query Match             76.0%;  Score 15.2;  DB 4;  Length 2399;
  Best Local Similarity   85.0%;  Pred. No. 4.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||| | ||||| |||
Db        831 GGTGCGTCCAGGCAGGAGGG 812


RESULT 14
US-08-477-460B-3/c
; Sequence 3, Application US/08477460B
; Patent No. 6034223
;  GENERAL INFORMATION:
;    APPLICANT:  Progenics Pharmaceuticals, Inc.
;    TITLE OF INVENTION:  NON-PEPTIDYL MOIETY-CONJUGATED
;    TITLE OF INVENTION:  CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,460B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/927,931
;      FILING DATE:  07-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41215-A-PCT/JPW/AJM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 977-9809
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2482 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      CELL TYPE:  lymphocyte
US-08-477-460B-3

  Query Match             76.0%;  Score 15.2;  DB 3;  Length 2482;
  Best Local Similarity   85.0%;  Pred. No. 4.5e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||| | ||||| |||
Db       1052 GGTGCGTCCAGGCAGGAGGG 1033


RESULT 15
US-08-379-516-3/c
; Sequence 3, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
;  APPLICANT: Allaway, Graham P.
;  APPLICANT: Maddon, Paul J.
;  TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
;  TITLE OF INVENTION: Immunoconjugates and Uses Thereof
;  FILE REFERENCE: 41215-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/08/379,516
;  CURRENT FILING DATE: 1996-06-10
;  EARLIER APPLICATION NUMBER: PCT/US93/07422
;  EARLIER FILING DATE: 1993-08-06
;  EARLIER APPLICATION NUMBER: 07/927,931
;  EARLIER FILING DATE: 1992-08-07
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2482
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-379-516-3
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Query Match 76.0%; Score 15.2; DB 3; Length 2482;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||| | ||||| |||
Db       1052 GGTGCGTCCAGGCAGGAGGG 1033
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Job time : 70.6385 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 268.243 Seconds
(without alignments)
453.893 Million cell updates/sec

Title: US-10-068-160A-31
Perfect score: 20
Sequence: 1 ggtgcgtcgacgcaggggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	14	US-10-068-160-31	Sequence 31, Appl
2	20	100.0	20	15	US-10-194-035-39	Sequence 39, Appl
3	20	100.0	20	15	US-10-194-035-41	Sequence 41, Appl
4	20	100.0	20	18	US-10-486-755-21	Sequence 21, Appl
5	20	100.0	20	19	US-10-499-597-19	Sequence 19, Appl
6	18.4	92.0	20	11	US-09-874-991C-498	Sequence 498, App
7	18.4	92.0	20	11	US-09-874-991C-509	Sequence 509, App
8	18.4	92.0	20	11	US-09-874-991C-542	Sequence 542, App
9	18.4	92.0	20	14	US-10-068-160-7	Sequence 7, Appli
10	18.4	92.0	20	14	US-10-068-160-35	Sequence 35, Appl
11	18.4	92.0	20	15	US-10-194-035-40	Sequence 40, Appl
12	18.4	92.0	20	15	US-10-194-035-81	Sequence 81, Appl
13	18.4	92.0	20	15	US-10-194-035-82	Sequence 82, Appl
14	18.4	92.0	20	15	US-10-194-035-100	Sequence 100, App
15	18.4	92.0	20	18	US-10-666-022-16	Sequence 16, Appl
16	18.4	92.0	20	18	US-10-486-755-4	Sequence 4, Appli
17	18.4	92.0	20	18	US-10-486-755-18	Sequence 18, Appl
18	18.4	92.0	20	18	US-10-486-755-20	Sequence 20, Appl
19	18.4	92.0	20	18	US-10-486-755-25	Sequence 25, Appl
20	18.4	92.0	20	19	US-10-499-597-14	Sequence 14, Appl
21	18.4	92.0	20	19	US-10-499-597-21	Sequence 21, Appl
22	18.4	92.0	28	11	US-09-874-991C-519	Sequence 519, App
23	18.4	92.0	28	11	US-09-874-991C-531	Sequence 531, App
24	18	90.0	18	14	US-10-068-160-14	Sequence 14, Appl
25	18	90.0	20	18	US-10-666-022-3	Sequence 3, Appli
26	18	90.0	20	18	US-10-486-755-7	Sequence 7, Appli
27	17.4	87.0	19	15	US-10-194-035-83	Sequence 83, Appl
28	17.4	87.0	19	15	US-10-194-035-88	Sequence 88, Appl
29	17	85.0	1272	17	US-10-425-114-24809	Sequence 24809, A
30	17	85.0	1836	18	US-10-425-115-167520	Sequence 167520,
31	16.8	84.0	20	11	US-09-874-991C-494	Sequence 494, App
32	16.8	84.0	20	11	US-09-874-991C-497	Sequence 497, App
33	16.8	84.0	20	11	US-09-874-991C-505	Sequence 505, App
34	16.8	84.0	20	11	US-09-874-991C-508	Sequence 508, App
35	16.8	84.0	20	11	US-09-874-991C-538	Sequence 538, App
36	16.8	84.0	20	11	US-09-874-991C-541	Sequence 541, App
37	16.8	84.0	20	14	US-10-068-160-1	Sequence 1, Appli
38	16.8	84.0	20	14	US-10-068-160-26	Sequence 26, Appl
39	16.8	84.0	20	14	US-10-068-160-54	Sequence 54, Appl
40	16.8	84.0	20	14	US-10-068-160-64	Sequence 64, Appl
41	16.8	84.0	20	15	US-10-194-035-32	Sequence 32, Appl
42	16.8	84.0	20	15	US-10-194-035-34	Sequence 34, Appl
43	16.8	84.0	20	15	US-10-194-035-37	Sequence 37, Appl
44	16.8	84.0	20	15	US-10-194-035-38	Sequence 38, Appl
45	16.8	84.0	20	15	US-10-194-035-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-10-068-160-31
; Sequence 31, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-31

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGTGCGTCGACGCAGGGGGG 20
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Db          1 GGTGCGTCGACGCAGGGGGG 20
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RESULT 2
US-10-194-035-39
; Sequence 39, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-39

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
||||||||||||||||||||
Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 3
US-10-194-035-41
; Sequence 41, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-41

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 4
US-10-486-755-21
; Sequence 21, Application US/10486755
; Publication No. US20040241841A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Mayda
; APPLICANT: Verhelyi, Daniela
; TITLE OF INVENTION: METHOD FOR RAPID GENERATION OF MATURE DENDRITIC CELLS
; FILE REFERENCE: 4239-67746
; CURRENT APPLICATION NUMBER: US/10/486,755
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: US 60/312,190
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: PCT/US02/25732
; PRIOR FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-486-755-21

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20
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Db 1 GGTGCGTCGACGCAGGGGGG 20

RESULT 5
US-10-499-597-19
; Sequence 19, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Rouse, Barry T.
; APPLICANT: Zheng, Mei
; TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
; FILE REFERENCE: 4239-64125-02
; CURRENT APPLICATION NUMBER: US/10/499,597
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: PCT/US02/40955
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/343,457
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG D oligonucleotide
US-10-499-597-19

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCGTCGACGCAGGGGGG 20

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                    ||||||||||||||||||||
Db          1 GGTGCGTCGACGCAGGGGGG 20


RESULT 6
US-09-874-991C-498
; Sequence 498, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-498

  Query Match             92.0%;  Score 18.4;  DB 11;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| |||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 7
US-09-874-991C-509
; Sequence 509, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-509

  Query Match             92.0%;  Score 18.4;  DB 11;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| |||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 8
US-09-874-991C-542
; Sequence 542, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-542

  Query Match             92.0%;  Score 18.4;  DB 11;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| |||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 9
US-10-068-160-7
; Sequence 7, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

  Query Match             92.0%;  Score 18.4;  DB 14;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 10
US-10-068-160-35
; Sequence 35, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
```

```
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-35

  Query Match             92.0%;  Score 18.4;  DB 14;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 11
US-10-194-035-40
; Sequence 40, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

  Query Match             92.0%;  Score 18.4;  DB 15;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 12
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

  Query Match             92.0%;  Score 18.4;  DB 15;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 13
US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

  Query Match             92.0%;  Score 18.4;  DB 15;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


RESULT 14
US-10-194-035-100
; Sequence 100, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
```

```
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-100

  Query Match             92.0%;  Score 18.4;  DB 15;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              ||||| ||||||||||||||
Db          1 GGTGCATCGACGCAGGGGGG 20


RESULT 15
US-10-666-022-16
; Sequence 16, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as represented by the
;  APPLICANT:  Secretary of the Department of Health and Human Services
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Verthelyi, Daniela
;  TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
;  TITLE OF INVENTION:  SUBJECTS WITH IMMUNOSTIMULATORY CPG
;  FILE REFERENCE: 4239-66899
;  CURRENT APPLICATION NUMBER: US/10/666,022
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: US 60/411,944
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 181
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-666-022-16

  Query Match             92.0%;  Score 18.4;  DB 18;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 29;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GGTGCGTCGACGCAGGGGGG 20
              |||||||||| |||||||||
Db          1 GGTGCGTCGATGCAGGGGGG 20


Search completed: April 29, 2005, 12:35:47
Job time : 268.243 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:31:54 ; Search time 633.081 Seconds
(without alignments)
1224.620 Million cell updates/sec

Title: US-10-068-160A-73
Perfect score: 16
Sequence: 1 actctggagcgttctc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15	93.8	657	8	AY294087	AY294087 Pinus mon
c	2	15	93.8	1125	6	BD165547	BD165547 Novel pol
c	3	15	93.8	1125	6	AX123430	AX123430 Sequence
c	4	15	93.8	1230	6	AX428867	AX428867 Sequence
c	5	15	93.8	1230	6	AX429521	AX429521 Sequence
	6	15	93.8	1753	8	ATCYC3B	Z31402 A.thaliana
c	7	15	93.8	2658	10	MMNETRN	Z32815 M.musculus
c	8	15	93.8	2945	8	AY735661	AY735661 Arabidops
c	9	15	93.8	101715	8	ATF4D11	AL022537 Arabidops
c	10	15	93.8	110992	8	ATF2I11	AL360314 Arabidops
	11	15	93.8	128789	2	AC113911	AC113911 Rattus no
	12	15	93.8	140057	1	BX927157	BX927157 Corynebac
c	13	15	93.8	142638	8	AP004750	AP004750 Oryza sat
	14	15	93.8	169260	2	AC132232	AC132232 Mus muscu
c	15	15	93.8	171061	10	AC119218	AC119218 Mus muscu
	16	15	93.8	172305	2	AC119639	AC119639 Rattus no
	17	15	93.8	176146	2	AC023124	AC023124 Homo sapi
	18	15	93.8	197252	8	ATCHRIV77	AL161581 Arabidops
	19	15	93.8	199450	9	AC005674	AC005674 Homo sapi
c	20	15	93.8	207184	9	AC012361	AC012361 Homo sapi
	21	15	93.8	215789	2	AC103449	AC103449 Rattus no
c	22	15	93.8	234627	2	AC106118	AC106118 Rattus no
	23	15	93.8	236455	2	AC135714	AC135714 Rattus no
	24	15	93.8	237078	2	AC094917	AC094917 Rattus no
c	25	15	93.8	240000	2	AC009528	AC009528 Homo sapi
	26	15	93.8	248106	2	AC126818	AC126818 Rattus no
	27	15	93.8	254169	2	AC127720	AC127720 Rattus no
	28	15	93.8	309400	6	AX127153	AX127153 Sequence
c	29	15	93.8	310029	1	AE016861	AE016861 Pseudomon
	30	15	93.8	325651	1	AP005283	AP005283 Corynebac
	31	14.4	90.0	16	6	AX194407	AX194407 Sequence
	32	14.4	90.0	16	6	AX352259	AX352259 Sequence
	33	14.4	90.0	16	6	AX352273	AX352273 Sequence
	34	14.4	90.0	16	6	AX352300	AX352300 Sequence
	35	14.4	90.0	16	6	AX465357	AX465357 Sequence
	36	14.4	90.0	17	6	AX194414	AX194414 Sequence
	37	14.4	90.0	17	6	AX465364	AX465364 Sequence
	38	14.4	90.0	18	6	AX104532	AX104532 Sequence
	39	14.4	90.0	18	6	AX194411	AX194411 Sequence
	40	14.4	90.0	18	6	AX355160	AX355160 Sequence
	41	14.4	90.0	18	6	AX465361	AX465361 Sequence
	42	14.4	90.0	18	6	AX547585	AX547585 Sequence
	43	14.4	90.0	19	6	AX194405	AX194405 Sequence
	44	14.4	90.0	19	6	AX352258	AX352258 Sequence
	45	14.4	90.0	19	6	AX352272	AX352272 Sequence

ALIGNMENTS

RESULT 1
AY294087/c
LOCUS AY294087 657 bp DNA linear PLN 12-DEC-2003
DEFINITION Pinus monticola putative NBS-LRR protein G6237 (RGA) gene, partial sequence.
ACCESSION AY294087
VERSION AY294087.1 GI:34099700
KEYWORDS .
SOURCE Pinus monticola (Western white pine)
ORGANISM Pinus monticola
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
REFERENCE 1 (bases 1 to 657)
AUTHORS Liu,J.-J. and Ekramoddoullah,A.K.M.
TITLE Isolation, genetic variation and expression of TIR-NBS-LRR resistance gene analogs from western white pine (Pinus monticola Dougl. ex. D. Don.)
JOURNAL Mol. Genet. Genomics 270 (5), 432-441 (2004)
PUBMED 14586641
REFERENCE 2 (bases 1 to 657)
AUTHORS Liu,J.-J. and Ekramoddoullah,A.K.M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2003) Natural Resources Canada, Pacific Forestry Centre, 506 West Burnside Road, Victoria, BC V8Z 1M5, Canada
FEATURES Location/Qualifiers
source 1. .657
/organism="Pinus monticola"
/mol_type="genomic DNA"
/db_xref="taxon:3345"
gene <1. .>657
/gene="RGA"
misc_feature <1. .>657
/gene="RGA"
/note="similar toputative NBS-LRR protein G6237; point mutation generates premature stop codon in NBS domain"
ORIGIN

Query Match 93.8%; Score 15; DB 8; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        193 CTCTGGAGCGTTCTC 179


RESULT 2
BD165547/c
LOCUS       BD165547               1125 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel polynucleotide.
ACCESSION   BD165547
VERSION     BD165547.1  GI:27871359
KEYWORDS    JP 2002191370-A/3346.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1125)
  AUTHORS   Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
  TITLE     Novel polynucleotide
  JOURNAL   Patent: JP 2002191370-A 3346 09-JUL-2002;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS   Corynebacterium glutamicum
            PN   JP 2002191370-A/3346
            PD   09-JUL-2002
            PF   15-DEC-2000 JP 2000405096
            PI   SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
            PI   KEIKO OCHIAI,
            PI   HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
            PI   OZAKI
            PC   C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00, PC
              C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/
            PC   04,C12P13/08,
            PC   C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
             G01N33/566,
            PC   G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
            PC   (C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00
            CC   Novel polynucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .1125
            FT                   /organism='Corynebacterium glutamicum'.
FEATURES              Location/Qualifiers
     source           1. .1125
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 6;  Length 1125;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        372 CTCTGGAGCGTTCTC 358


RESULT 3
AX123430/c
LOCUS       AX123430               1125 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 3346 from Patent EP1108790.
ACCESSION   AX123430
VERSION     AX123430.1  GI:14040918
KEYWORDS    .
SOURCE      Corynebacterium glutamicum
  ORGANISM  Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1
  AUTHORS   Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
  TITLE     Novel polynucleotides
  JOURNAL   Patent: EP 1108790-A 3346 20-JUN-2001;
            KYOWA HAKKO KOGYO CO., LTD. (JP)
FEATURES              Location/Qualifiers
     source           1. .1125
                      /organism="Corynebacterium glutamicum"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:1718"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 6;  Length 1125;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        372 CTCTGGAGCGTTCTC 358


RESULT 4
AX428867/c
LOCUS       AX428867               1230 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 3 from Patent EP1202065.
ACCESSION   AX428867
VERSION     AX428867.1  GI:21540259
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Wasylyk,B., Multon,M.C., Ayadi,A. and Zheng,H.
  TITLE     Net, a transcription factor of the tcf family, as regulator of
            angiogenic expression
  JOURNAL   Patent: EP 1202065-A 3 02-MAY-2002;
            Aventis Pharma S.A. (FR) ; INSERM (FR)
FEATURES              Location/Qualifiers
     source           1. .1230
                      /organism="Mus musculus"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:10090"
     CDS              1. .1230
                      /note="unnamed protein product; Sequence of NET
                      transcription factor"
                      /codon_start=1
                      /protein_id="CAD36073.1"
                      /db_xref="GI:21540260"
                      /translation="MESAITLWQFLLHLLLDQKHEHLICWTSNDGEFKLLKAEEVAKL
                      WGLRKNKTNMNYDKLSRALRYYYDKNIIKKVIGQKFVYKFVSFPDILKMDPHAVEISR
                      ESLLLQDGDCKVSPEGREVHRHGLSSLKSASRNEYLHSGLYSSFTINSLENAPEAFKA
                      IKTEKLEEPCDDSPPVEEVRTVIRFVTNKTDKHITRPVMSLPSTSETAAAAASAFLAS
                      SVSAKISSLMLPNAASVSSVSPSSSRSPSLSPDSPLPSEHRSLFLEAACHESDSLEPL
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                      AQTPSGLFLASSPLLPSIHFWSSLSPVAPLSPARLQGPNTLFQFPTLLNGHMPVPLPS
                      LDRAPSPVLLSPSSQKS"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 6;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        468 CTCTGGAGCGTTCTC 454


RESULT 5
AX429521/c
LOCUS       AX429521               1230 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 3 from Patent WO0235235.
ACCESSION   AX429521
VERSION     AX429521.1  GI:21540795
KEYWORDS    .
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SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Wasylyk,B., Zheng,H., Ayadi,A. and Multon,M.C.
  TITLE     Net, a transcription factor of the tcf family, as regulator of
            angiogenic expression
  JOURNAL   Patent: WO 0235235-A 3 02-MAY-2002;
            AVENTIS PHARMA SA (FR); INST NAT SANTE RECH MED (FR)
FEATURES             Location/Qualifiers
     source          1. .1230
                     /organism="Mus musculus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10090"
     CDS             1. .1230
                     /note="unnamed protein product; Sequence of NET
                     transcription factor"
                     /codon_start=1
                     /protein_id="CAD36125.1"
                     /db_xref="GI:21540796"
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                     ESLLLQDGDCKVSPEGREVHRHGLSSLKSASRNEYLHSGLYSSFTINSLENAPEAFKA
                     IKTEKLEEPCDDSPPVEEVRTVIRFVTNKTDKHITRPVMSLPSTSETAAAAASAFLAS
                     SVSAKISSLMLPNAASVSSVSPSSSRSPSLSPDSPLPSEHRSLFLEAACHESDSLEPL
                     NLSSGSKTKSPSLPPKGKKPKGLEISAPQLLLSGTDIGSIALNSPALPSGSLTPAFFT
                     AQTPSGLFLASSPLLPSIHFWSSLSPVAPLSPARLQGPNTLFQFPTLLNGHMPVPLPS
                     LDRAPSPVLLSPSSQKS"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 6;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        468 CTCTGGAGCGTTCTC 454


RESULT 6
ATCYC3B
LOCUS       ATCYC3B                 1753 bp    mRNA    linear   PLN 21-APR-1995
DEFINITION  A.thaliana (Columbia) cyc3b mRNA for cyclin 3b protein.
ACCESSION   Z31402
VERSION     Z31402.1  GI:728520
KEYWORDS    cyc3b gene; cyclin 3b.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1752)
  AUTHORS   Ferreira,P., Hemerly,A., de Almeida Engler,J., Bergounioux,C.,
            Burssens,S., Van Montagu,M., Engler,G. and Inze,D.
  TITLE     Three discrete classes of Arabidopsis cyclins are expressed during
            different intervals of the cell cycle
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (24), 11313-11317 (1994)
  MEDLINE   95062258
   PUBMED   7972055
REFERENCE   2
  AUTHORS   Van Montagu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-1994) Van Montagu M., Rijksuniverisiteit Gent,
            Laboratory of Genetics, Ledeganckstraat, 35, Gent, Belgium, B-9000
  REMARK    revised by [4]   MAT
REFERENCE   3  (bases 1 to 1753)
  AUTHORS   Van Montagu,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAR-1995) Van Montagu M., Rijksuniverisiteit Gent,
            Laboratory of Genetics, Ledeganckstraat, 35, Gent, Belgium, B-9000
COMMENT     On Mar 25, 1995 this sequence version replaced gi:509426.
FEATURES             Location/Qualifiers
     source          1. .1753
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="cyc3bAt"
                     /tissue_type="cell suspensions"
                     /clone_lib="cell suspension lambda ZapII"
     gene            1. .1753
                     /gene="cyc3b"
     CDS             141. .1451
                     /gene="cyc3b"
                     /codon_start=1
                     /product="cyclin 3b"
                     /protein_id="CAA83277.1"
                     /db_xref="GI:784946"
                     /db_xref="GOA:Q39073"
                     /db_xref="UniProt/TrEMBL:Q39073"
                     /translation="MYCSSSMHPNANKENISTSDVQESFVRITRSRAKKAMGRGVSIP
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                     DILVDMHTEKSKLAEDLSKIRMAEAQDVSLSNFKDEEITEQQEDGSGVMELLQVVDID
                     SNVEDPQCCSLYAADIYDNIHVAELQQRPLANYMELVQRDIDPDMRKILIDWLVEVSD
                     DYKLVPDTLYLTVNLIDRFLSNSYIERQRLQLLGVSCMLIASKYEELSAPGVEEFCFI
                     TANTYTRREVLSMEIQILNFVHFRLSVPTTKTFLRRFIKAAQASYKVPFIELEYLANY
                     LAELTLVEYSFLRFLPSLIAASAVFLARWTLDQTDHPWNPTLQHYTRYEVAELKNTVL
                     AMEDLQLNTSGCTLAATREKYNQPKFKSVAKLTSPKRVTLLFSR"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 8;  Length 1753;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db         18 CTCTGGAGCGTTCTC 32


RESULT 7
MMNETRN/c
LOCUS       MMNETRN                 2658 bp    mRNA    linear   ROD 13-MAR-1995
DEFINITION  M.musculus net mRNA.
ACCESSION   Z32815
VERSION     Z32815.1  GI:479112
KEYWORDS    Net; ras gene.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2658)
  AUTHORS   Giovane,A., Pintzas,A., Maira,S.M., Sobieszczuk,P. and Wasylyk,B.
  TITLE     Net, a new ets transcription factor that is activated by Ras
  JOURNAL   Genes Dev. 8 (13), 1502-1513 (1994)
  MEDLINE   95047310
   PUBMED   7958835
REFERENCE   2  (bases 1 to 2658)
  AUTHORS   Giovane,A., Pintzas,A., Maira,S.M., Sobieszczuk,P. and Wasylyk,B.
  TITLE     Net, a negative factor switch to positive by Ras
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2658)
  AUTHORS   Giovane,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-1994) Antoine Giovane,
            CNRS-LGME,INSERM-U.184,institut de Chimie, Biologique, 11 rue
            Humann, Strasbourg, 67085 Strasb. Cedex, France
FEATURES             Location/Qualifiers
     source          1. .2658
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /tissue_type="embryo"
                     /clone_lib="lambda zap2"
                     /dev_stage="10 days"
     CDS             295. .1524
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                     /product="Net"
                     /protein_id="CAA83676.1"
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                     /db_xref="GOA:P41971"
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                     IKTEKLEEPCDDSPPVEEVRTVIRFVTNKTDKHITRPVMSLPSTSETAAAAASAFLAS
                     SVSAKISSLMLPNAASVSSVSPSSSRSPSLSPDSPLPSEHRSLFLEAACHESDSLEPL
                     NLSSGSKTKSPSLPPKGKKPKGLEISAPQLLLSGTDIGSIALNSPALPSGSLTPAFFT
                     AQTPSGLFLASSPLLPSIHFWSSLSPVAPLSPARLQGPNTLFQFPTLLNGHMPVPLPS
                     LDRAPSPVLLSPSSQKS"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 10;  Length 2658;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        762 CTCTGGAGCGTTCTC 748


RESULT 8
AY735661/c
LOCUS       AY735661               2945 bp    mRNA    linear   PLN 26-SEP-2004
DEFINITION  Arabidopsis thaliana hypothetical protein AT4G32670 mRNA, complete
            cds.
ACCESSION   AY735661
VERSION     AY735661.1  GI:52354420
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2945)
  AUTHORS   Xiao,Y., Underwood,B., Moskal,W., Wang,W., Redman,J., Wu,H.C.,
            Utterback,T. and Town,C.D.
  TITLE     Reconstruction of cDNA sequences for hypothetical genes in
            Arabidopsis thaliana from 5' and 3' RACE products
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2945)
  AUTHORS   Xiao,Y., Underwood,B., Moskal,W., Wang,W., Redman,J., Wu,H.C.,
            Utterback,T. and Town,C.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2004) Plant Genomics, The Institute for Genomic
            Research, 9712 Medical Center Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .2945
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="4"
                     /ecotype="Columbia"
     CDS             79. .2661
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                     /evidence=not_experimental
                     /product="hypothetical protein AT4G32670"
                     /protein_id="AAU44531.1"
                     /db_xref="GI:52354421"
                     /translation="MXISPAEDKLVGSGEAVTTEEVSDINNKAVDICRICQSPEEPDN
                     PLRHPCACRGSLKYIHSDCLFLWLNRRKRNHCEICKRSYSIVPVYSENAPERLPWHEF
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                     AQIVSSATEMVVQMETIRVLLRRHPEFLRRMIILENGLKDRDVTGIVLLLANHLQILC
                     DWWHDQLLQLPFLHIFQRGPLALAFVPRNTPLHQFGAIRRVFSLLSDNTFAVLAINIY
                     WSFFRVLLPFSIGRVVLVLLRCLPHGWIAENASEMAAGDMVIRSVLLACLGGVFTMSR
                     DTYLTSVRTFLPSVKDTFILSFKLGVLPWLLGCWLHFCTFPILGKTASHTVEVLSDYP
                     LMADKHWLMGTLYLVSALSCMELIQKIVQKRALWYLLDVAEPNYKVTKLHLGPILLAF
                     ALHGTMVVIVLHLPIKTISLISQSFFPLQFGVYEDEFVFGLLVAYMCLVIFGPRWLAN
                     LIRPSIRPIVHKWVITISSLLKLSDFLLGEPRKHRANHNMRLRCLVFGIAEGSMVSLH
                     GSQSDTTCEKDTNEQRDKRFMVRIGVMLILASLSMFLVSTTFMALPILVGRAFFHSIS
                     FFMLSFGLKHDDLCAFWIGFCILRGIYIITCFVYDHFITGRTDLLLNHVLMFIRNVLL
                     FSIWISVIPGVLGLLIDLMIIIPSQVPLGESPVYNLLHDWLIGVVVLHIWIFLTMLTR
                     INCFATVAWREKLQRIRSVTINRLPFTWLIRDVIGSIIVSLLFTLCVPYVVVNSLFPI
                     LGFSSAVNLTVQRFIWPAILALIPIWFSVKLIRDLILYLHKLEFDNRYKVGERLVDFT
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     misc_difference 807
                     /note="mismatch relative to genomic"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 8;  Length 2945;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        363 CTCTGGAGCGTTCTC 349


RESULT 9
ATF4D11/c
LOCUS       ATF4D11               101715 bp    DNA     linear   PLN 27-AUG-1999
DEFINITION  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII
            project).
ACCESSION   AL022537
VERSION     AL022537.1  GI:3063690
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Bevan,M., Benes,V., Rechmann,S., Borkova,D., Ansorge,W.,
            Hoheisel,J., Mewes,H.W., Mayer,K.F.X. and Schueller,C.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 101715)
  AUTHORS   EU Arabidopsis sequencing,project.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-1998) MIPS, at the Max-Planck-Institut fuer
            Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project
            Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
            Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
            E-mail: michael.bevan@bbsrc.ac.uk
FEATURES             Location/Qualifiers
     source          1. .101715
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /variety="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="4"
     gene            2154. .4496
                     /gene="F4D11.10"
     gene            complement(join(2154. .2813,2909. .3257,3625. .3755,
                     3855. .4496))
                     /gene="F4D11.10"
     CDS             complement(join(2154. .2813,2909. .3257,3625. .3755,
                     3855. .4496))
                     /gene="F4D11.10"
                     /note="similarity to multiple exostosis 2, Homo sapiens"
                     /codon_start=1
                     /product="putative protein"
                     /protein_id="CAA18582.1"
                     /db_xref="GI:3063691"
                     /db_xref="GOA:O65522"
                     /db_xref="UniProt/TrEMBL:O65522"
                     /translation="MLNLWLREHLVYVCHQQNLVAKFRSQKAMKLLRFAGLVFIFITT
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                     NIRKMEILESKSDPSVDNLSSEVKKFMNVSNSGVVSITEMMNLLHQSRTSHVSLKVKR
                     SSTIDHELLYARTQIENPPLIENDPLLHTPLYWNLSMFKRSYELMEKKLKVYVYREGK
                     RPVLHKPVLKGIYASEGWFMKQLKSSRTFVTKDPRKAHLFYLPFSSKMLEETLYVPGS
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intron          complement(2814. .2908)
                /gene="F4D11.10"
                /number=1
exon            complement(2909. .3257)
                /gene="F4D11.10"
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intron          complement(3258. .3624)
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exon            complement(3625. .3755)
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                /number=3
intron          complement(3756. .3854)
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                /number=3
exon            complement(3855. .4496)
                /gene="F4D11.10"
                /number=4
gene            6155. .8136
                /gene="F4D11.20"
gene            complement(join(6155. .6547,7111. .7176,7846. .8006,
                8082. .8136))
                /gene="F4D11.20"
CDS             complement(join(6155. .6547,7111. .7176,7846. .8006,
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                /gene="F4D11.20"
                /note="similarity to predicted proteins, Arabidopsis
                thaliana
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                contains EST gb:AA395096, T42550"
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                IYCFLA"
exon            complement(6155. .6547)
                /gene="F4D11.20"
                /number=1
intron          complement(6548. .7110)
                /gene="F4D11.20"
                /number=1
exon            complement(7111. .7176)
                /gene="F4D11.20"
                /number=2
intron          complement(7177. .7845)
                /gene="F4D11.20"
                /number=2
exon            complement(7846. .8006)
                /gene="F4D11.20"
                /number=3
intron          complement(8007. .8081)
                /gene="F4D11.20"
                /number=3
exon            complement(8082. .8136)
                /gene="F4D11.20"
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gene            9271. .11609
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                10008. .10115,10239. .10336,10486. .10655,10768. .10844,
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                /db_xref="GOA:Q94FY7"
                /db_xref="UniProt/Swiss-Prot:Q94FY7"
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                YAETVKSARWEYSTRPVYGWGDVGAKQKSTAGWPAAFPVFEPHWQICMAGGLSTGWIE
                WGGERFEFRDAPSYSEKNWGGGFPRKWFWVQCNVFEGATGEVALTAGGGLRQLPGLTE
                TYENAALVCVHYDGKMYEFVPWNGVVRWEMSPWGYWYITAENENHVVELEARTNEAGT
                PLRAPTTEVGLATACRDSCYGELKLQIWERLYDGSKGKLKVLTNPKAVKEDYERLLWL
                TMMQVILETKSSMAAVEIGGGPWFGTWKGDTSNTPELLKQALQVPLDLESALGLVPFF
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exon            complement(9271. .9522)
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intron          complement(9523. .9554)
                /gene="F4D11.30"
                /number=1
exon            complement(9555. .9704)
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                /number=2
intron          complement(9705. .9800)
                /gene="F4D11.30"
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intron          complement(9918. .10007)
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                /number=3
exon            complement(10008. .10115)
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                /gene="F4D11.30"
                /number=4
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intron          complement(10337. .10485)
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exon            complement(10486. .10655)
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Qy          2 CTCTGGAGCGTTCTC 16
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Db      54640 CTCTGGAGCGTTCTC 54626


RESULT 10
ATF2I11/c
LOCUS       ATF2I11                 110992 bp    DNA     linear   PLN 05-JUL-2000
DEFINITION  Arabidopsis thaliana DNA chromosome 5, BAC clone F2I11 (ESSA
            project).
ACCESSION   AL360314
VERSION     AL360314.1  GI:8953373
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 3355)
  AUTHORS   Bevan,M., Volckaert,G., Grymonprez,B., Voet,M., Robben,J.,
            Bancroft,I., Mewes,H.W., Rudd,S., Lemcke,K. and Mayer,K.F.X.
  JOURNAL   Unpublished
REFERENCE   2  (bases 2885 to 110992)
  AUTHORS   Bevan,M., Peters,S.A., van Staveren,M., Dirkse,W., Stiekema,W.,
            Bancroft,I., Mewes,H.W., Rudd,S., Lemcke,K. and Mayer,K.F.X.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 110992)
  AUTHORS   EU Arabidopsis sequencing,project.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-2000) MIPS, at the Max-Planck-Institut fuer
            Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
            lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
            Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
            Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
            E-mail: michael.bevan@bbsrc.ac.uk
COMMENT     Information on performance of analysis and a more detailed
            annotation of this entry and other sequences of chromosomes 3, 4
            and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
FEATURES             Location/Qualifiers
     source          1. .110992
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                     /mol_type="genomic DNA"
                     /variety="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="5"
     gene            5081. .5751
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     CDS             join(5081. .5302,5485. .5751)
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                     IRKAGEKNLRRDRDRTNNSDVGVVSNGSVYLNAFTFHQLRPFLSPHFFPIFAYSLSLF
                     SL"
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                     /number=1
     intron          5303. .5484
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                     /number=1
     exon            5485. .5751
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                     /note="similarity to various predicted proteins,
                     Arabidopsis thaliana"
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                     GFVHTGEPPQNRKLLAFFAGGSHGDVRKILFQHWKEKDKDVLVYENLPKTMNYTKMMD
                     KAKFCLCPSGWEVASPRIVESLYSGCVPVIIADYYVLPFSDVLNWKTFSVHIPISKMP
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     exon            6817. .7485
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     CDS             8104. .8829
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                     AVMEKKAGEHRLLLAKQEMELSLKKLAEKEKEMKEFREKLMKTTGKLGSLEMKRTCLD
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     CDS             complement(join(9386. .9476,9672. .9835,9993. .10183,
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                     /db_xref="UniProt/Swiss-Prot:Q9LFP1"
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                     DKTENMQGNTFRFRKQARRYRTIMWWRNVKLTIALILVLALVVYIAMAFVCHGPSLPS
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                14464. .14522,14676. .14747)
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                /note="strong similarity to adenine
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                EMBL:ATAPT2GEN"
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                /db_xref="UniProt/TrEMBL:Q9LFP0"
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     intron     14523. .14675
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Query Match             93.8%;  Score 15;  DB 8;  Length 110992;
Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
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Db      68011 CTCTGGAGCGTTCTC 67997


RESULT 11
AC113911
LOCUS       AC113911              128789 bp    DNA     linear   HTG 19-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-393O22, *** SEQUENCING IN PROGRESS
            ***.
ACCESSION   AC113911
VERSION     AC113911.5  GI:25072582
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 128789)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
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            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
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            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
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            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
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            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 128789)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
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  JOURNAL   Submitted (05-MAR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 128789)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 19, 2002 this sequence version replaced gi:23815605.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GTDK
                Center clone name: CH230-393O22
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 124060 bases at least Q40
                Consensus quality: 125303 bases at least Q30
                Consensus quality: 126081 bases at least Q20
                Estimated insert size: 125161; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   128789: contig of 128789 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-393O22"
     misc_feature    1. .1287
                     /note="wgs_end_extension
                     clone_end:T7"
     misc_feature    1338. .3296
                     /note="wgs_end_extension
                     clone_end:T7"
     misc_feature    complement(5045. .5957)
                     /note="clone_boundary
                     clone_end:T7
                     site:
                     end_sequence:BZ125599"
     misc_feature    87889. .89007
                     /note="wgs_contig"
     misc_feature    complement(124228. .125002)
                     /note="clone_boundary
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                     site:
                     end_sequence:BZ125600"
     misc_feature    125406. .126558
                     /note="wgs_end_extension
                     clone_end:Sp6"
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                     /note="wgs_end_extension
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ORIGIN

  Query Match             93.8%;  Score 15;  DB 2;  Length 128789;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCT 15
              |||||||||||||||
Db      14490 ACTCTGGAGCGTTCT 14504


RESULT 12
BX927157
LOCUS       BX927157               140057 bp    DNA     linear   BCT 10-JUN-2004
DEFINITION  Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5,
            complete genome; segment 10/10.
ACCESSION   BX927157 BX927147
VERSION     BX927157.1  GI:41222957
KEYWORDS    complete genome.
SOURCE      Corynebacterium glutamicum ATCC 13032
  ORGANISM  Corynebacterium glutamicum ATCC 13032
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1  (bases 1 to 140057)
  AUTHORS   Kalinowski,J., Bathe,B., Bartels,D., Bischoff,N., Bott,M.,
            Burkovski,A., Dusch,N., Eggeling,L., Eikmanns,B.J., Gaigalat,L.,
            Goesmann,A., Hartmann,M., Huthmacher,K., Kramer,R., Linke,B.,
            McHardy,A.C., Meyer,F., Mockel,B., Pfefferle,W., Puhler,A.,
            Rey,D.A., Ruckert,C., Rupp,O., Sahm,H., Wendisch,V.F., Wiegrabe,I.
            and Tauch,A.
  TITLE     The complete Corynebacterium glutamicum ATCC 13032 genome sequence
            and its impact on the production of L-aspartate-derived amino acids
            and vitamins
  JOURNAL   J. Biotechnol. 104 (1-3), 5-25 (2003)
  MEDLINE   22830012
   PUBMED   12948626
REFERENCE   2  (bases 1 to 140057)
  AUTHORS   Kalinowski,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer
            Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,
            33615 Bielefeld, Germany
            E-mail:Joern.Kalinowski@Cebitec.Uni-Bielefeld.DE
COMMENT     This sequence was accomplished by collaboration between Degussa AG
            and Bielefeld University.
            join(BX927148.1:1. .348071,BX927149.1:51. .349887,
            BX927150.1:51. .348475,
            BX927151.1:51. .349459,BX927152.1:51. .349799,BX927153.1:51. .349584,
            BX927154.1:51. .349575,BX927155.1:51. .349136,BX927156.1:51. .349115,
            BX927157.1:51. .140057).
FEATURES             Location/Qualifiers
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                     /strain="DSM 20300 = ATCC 13032"
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                     /note="IS fingerprint type: 4-5"
     gene            70. .1551
                     /locus_tag="cg3287"
     CDS             70. .1551
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                     /transl_table=11
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                     /db_xref="GI:41222958"
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                     RGLHAPLIIRDPQDAEDQDVEWTIVLDDWVDGIQGTPDDELDKLTGMGSGDHNGRMGM
                     GGHGQMMHGTPDRVLGGDVGDVMYPHYLINGRIPRAHRTFEARPGDKARLRFINSGGD
                     TIFKVALGGHRMTVTHTDGFPVQPWETESIYLSMGERVDVEVILGDGIFPLTALAVGK
                     DDRAFAVIRTAGGQAPRPDVDFPELSSTGLLLSSLKPADRALLPEGTPDREVSIDLGG
                     QMMPYEWSILTDGQSSSATVQEGQRLRMVMRNRTMMPHPMHIHGHTWALPGSGGLRKD
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gene                 1578. .1688
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CDS                  1578. .1688
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CDS                  1910. .2275
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                     /db_xref="GI:41222960"
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                     DRSHRPAAVFLREVTALSG"
gene                 complement(2272. .3192)
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CDS                  complement(2272. .3192)
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                     /transl_table=11
                     /product="PROBABLE OXIDOREDUCTASE PROTEIN"
                     /protein_id="CAF18906.1"
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                     /translation="MSKVYVSNEYGGPENQELITRNTPQPGPGELGVKVHAAGVNPLD
                     WKVRSGVAGTPRELPAPLGEEASGIVTAVGDGVEGFAVGDPVLGLVAPGVGGYAEDTL
                     LVAESTVLKPEEISFTDAAAIPVAGASAYAGTHQVELEPGQSLLINGAGGGVGLMAAQ
                     IGRVHKFQVVGVDHEDKRELIESTGAIFVATGDAVAEQVRALLPDGVDVVFDLVGGEA
                     LRVVAPLAKNPAHVISAADAATVGELGGQVLRRTPEMVGQITGVVQYGLVDPKVDTTY
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                     /db_xref="GI:41222962"
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gene                 4280. .4516
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CDS                  4280. .4516
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                     /transl_table=11
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gene                 4722. .5039
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CDS                  4722. .5039
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gene                 complement(5437. .5550)
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CDS                  complement(5437. .5550)
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                     /transl_table=11
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gene                 5683. .7560
                     /locus_tag="cg3295"
CDS                  5683. .7560
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                     ALSDLVDAAPETATVLRDGEPETVEIWELAPGDVVLVKNGEQIPVDGRVLSGHGGVDE
                     ATITGESVPAEKAADSEVFAGTWLRSGVLRIEAIGIGSDSTLAKIIHRVEDAQDDKAK
                     TQTFLEKFSKYYTPGVMIAALAVGLITLNVELALTLLVIACPGALVISIPVSIVAGIG
                     RSAKDGVLIKGGEYLETSAKVDTVVVDKTGTLTNGRPELTNVDVLDPAYSDDEVLTLA
                     ARAETASEHPLAEAIIRGAENRGLTVAMVEKAEPVAGRGIRADVDGATVAVGSADLLD
                     HTPDNTRILELNEQGRTAMYVGINGKAVGIVAVADTIRDDAPAAIRSLHNKGIRVVMA
                     TGDAERVARNVAAELGVDEVRAELMPEDKLEIVKELQAQGRVVAMVGDGVNDTPALAT
                     ADIGVAMGAAGSPAAIETADIALMADKLPRLPYALGLAQRTVRTMRVNIGIALLTVTI
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CDS                  complement(7742. .7960)
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                     AERARHDVCPHGQPNPDAVIVNRVFETA"
gene                 complement(7961. .8221)
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                     /locus_tag="cg3297"
CDS                  complement(7961. .8221)
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                     /locus_tag="cg3297"
                     /codon_start=1
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                     /protein_id="CAF18913.1"
                     /db_xref="GI:41222968"
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                     ALRSNASAGYPRVINTDKAPSLARAITELKSEGICPPTVEHR"
gene                 complement(8178. .8339)
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                     /locus_tag="cg3298"
CDS                  complement(8178. .8339)
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  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
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Db      56973 CTCTGGAGCGTTCTC 56987


RESULT 13
AP004750/c
LOCUS       AP004750               142638 bp    DNA     linear   PLN 29-APR-2004
DEFINITION  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
            PAC clone:P0421H01, complete sequence.
ACCESSION   AP004750
VERSION     AP004750.2  GI:46849606
KEYWORDS    HTG.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
            clone:P0421H01
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 142638)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2002) Takuji Sasaki, National Institute of
            Agrobiological Sciences, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     On Apr 28, 2004 this sequence version replaced gi:18656396.
            The orientation of the sequence is from T7 to SP6 of the PAC clone.
FEATURES             Location/Qualifiers
     source          1. .142638
                     /organism="Oryza sativa (japonica cultivar-group)"
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                     /db_xref="taxon:39947"
                     /chromosome="6"
                     /clone="P0421H01"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCT 15
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Db      23348 ACTCTGGAGCGTTCT 23334


RESULT 14
AC132232
LOCUS       AC132232               169260 bp    DNA     linear   HTG 10-JUL-2004
DEFINITION  Mus musculus chromosome 10 clone RP24-489N16, WORKING DRAFT
            SEQUENCE, 4 unordered pieces.
ACCESSION   AC132232
VERSION     AC132232.4  GI:49406093
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 169260)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Mus musculus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 169260)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   3  (bases 1 to 169260)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2004) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
COMMENT     On Jun 29, 2004 this sequence version replaced gi:38229484.

            ---------------- Genome Center ----------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            -------------- Project Information -------------------
            Center project name: M_BB0489N16
            ------------------------------------------------------
            -------------- Summary Statistics  -------------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 166593 bases at least Q40
            Consensus quality: 167225 bases at least Q30
            Consensus quality: 167677 bases at least Q20
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    83676: contig of 83676 bp in length
            *    83677    83776: gap of unknown length
            *    83777    84899: contig of 1123 bp in length
            *    84900    84999: gap of unknown length
            *    85000   110130: contig of 25131 bp in length
            *   110131   110230: gap of unknown length
            *   110231   169260: contig of 59030 bp in length.
FEATURES             Location/Qualifiers
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                     /chromosome="10"
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     misc_feature    83777. .84899
                     /note="assembly_name:Contig4"
     misc_feature    85000. .110130
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     misc_feature    110231. .169260
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ORIGIN

  Query Match             93.8%;  Score 15;  DB 2;  Length 169260;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCT 15
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Db      86239 ACTCTGGAGCGTTCT 86253
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RESULT 15
AC119218/c
LOCUS       AC119218              171061 bp    DNA     linear   ROD 15-JUN-2004
DEFINITION  Mus musculus chromosome 7, clone RP24-200I20, complete sequence.
ACCESSION   AC119218
VERSION     AC119218.7  GI:48717606
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 171061)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 7, clone RP24-200I20
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171061)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
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            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 171061)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
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            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
            Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
            MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
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            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
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            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   4  (bases 1 to 171061)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
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            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
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            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
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            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUN-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jun 15, 2004 this sequence version replaced gi:46358182.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@broad.mit.edu
            -------------- Project Information
                Center project name: L25218
                Center clone name: 200_I_20
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Job time : 637.206 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 04:24:29 ; Search time 163.135 Seconds
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Perfect score: 16
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	16	10	ADD01091	Add01091 CpG K oli
c 2	15	93.8	1125	5	AAH68311	Aah68311 C glutami
c 3	15	93.8	1230	6	ABK85615	Abk85615 DNA encod
c 4	15	93.8	2979	10	ADE61030	Ade61030 Human gen
c 5	15	93.8	2979	10	ADE61034	Ade61034 Human gen
6	15	93.8	309400	5	AAH68534	Aah68534 C glutami
7	14.4	90.0	16	4	AAC80587	Aac80587 Immunogen
8	14.4	90.0	16	4	AAS09557	Aas09557 Immunorea
9	14.4	90.0	16	6	ABL35643	Abl35643 Immunosti
10	14.4	90.0	16	6	ABL35670	Abl35670 Immunosti
11	14.4	90.0	16	6	ABL35629	Abl35629 Immunosti
12	14.4	90.0	16	6	ABK46435	Abk46435 Immunosti
13	14.4	90.0	16	9	ACC83067	Acc83067 K class C
14	14.4	90.0	16	10	ADD01102	Add01102 CpG K oli
15	14.4	90.0	17	4	AAC80594	Aac80594 Immunogen
16	14.4	90.0	17	4	AAS09564	Aas09564 Immunorea
17	14.4	90.0	17	6	ABK46442	Abk46442 Immunosti
18	14.4	90.0	17	9	ACC83066	Acc83066 K class C
19	14.4	90.0	18	4	AAC80591	Aac80591 Immunogen
20	14.4	90.0	18	4	AAF99525	Aaf99525 Immunosti
21	14.4	90.0	18	4	AAS09561	Aas09561 Immunorea
22	14.4	90.0	18	6	ABS78240	Abs78240 Angiogene
23	14.4	90.0	18	6	ABL38807	Abl38807 Immunosti
24	14.4	90.0	18	6	ABK46439	Abk46439 Immunosti
25	14.4	90.0	18	9	ACC83065	Acc83065 K class C
26	14.4	90.0	18	9	ACH03062	Ach03062 Immunosti
27	14.4	90.0	18	9	ADB37027	Adb37027 Immunosti
28	14.4	90.0	19	4	AAC80585	Aac80585 Immunogen
29	14.4	90.0	19	4	AAS09555	Aas09555 Immunorea
30	14.4	90.0	19	6	ABL35628	Abl35628 Immunosti
31	14.4	90.0	19	6	ABL35669	Abl35669 Immunosti
32	14.4	90.0	19	6	ABL35642	Abl35642 Immunosti
33	14.4	90.0	19	6	ABK46433	Abk46433 Immunosti
34	14.4	90.0	19	9	ACC83064	Acc83064 K class C
35	14.4	90.0	19	10	ADD01095	Add01095 CpG K oli
36	14.4	90.0	20	2	AAV27685	Aav27685 Immunosti
37	14.4	90.0	20	2	AAV27683	Aav27683 Immunosti
38	14.4	90.0	20	2	AAV72501	Aav72501 CpG motif
39	14.4	90.0	20	2	AAZ41862	Aaz41862 IL-12 sec
40	14.4	90.0	20	2	AAZ41864	Aaz41864 IL-12 sec
41	14.4	90.0	20	2	AAZ41865	Aaz41865 IL-12 sec
42	14.4	90.0	20	2	AAZ41886	Aaz41886 IL-12 sec
43	14.4	90.0	20	2	AAZ41883	Aaz41883 IL-12 sec
44	14.4	90.0	20	2	AAZ41863	Aaz41863 IL-12 sec
45	14.4	90.0	20	3	AAZ60939	Aaz60939 Nucleotid

ALIGNMENTS

RESULT 1
ADD01091
ID ADD01091 standard; DNA; 16 BP.
XX
AC ADD01091;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG K oligonucleotide SEQ ID NO:55.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerary; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
PN WO2003054161-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Zheng M, Rouse BT;
XX
DR WPI; 2003-559138/52.
XX
PT Inducing the production of vascular endothelial growth factor by a cell,
PT useful for inducing angiogenesis, comprises contacting the cell with a
PT CpG oligodeoxynucleotide.
XX
PS Example 7; SEQ ID NO 55; 37pp; English.
XX
CC The present invention describes a method for inducing the production of
CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC the cell with a CpG oligonucleotide and therefore inducing the production
CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC tissue, comprising introducing a CpG oligonucleotide into an area of the

CC tissue where the formation of new blood vessels is desired, and so
CC inducing neovascularisation in the area of the tissue; (2) promoting
CC angiogenesis in an area of the subject where angiogenesis is desired,
CC comprising introducing a CpG oligonucleotide to the area, and so
CC promoting angiogenesis in the subject; and (3) screening for an agent
CC that inhibits neovascularisation, comprising administering a CpG
CC oligonucleotide to a non-human mammal and administering the agent to the
CC mammal, where inhibition of angiogenesis in the animal indicates that the
CC agent is effective in inhibiting neovascularisation. The CpG
CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC activities, and can be used in gene therapy. The method and the CpG
CC oligonucleotides can be used in inducing angiogenesis or
CC neovascularisation, such as in subjects with a skin graft, subjects who
CC exhibit male pattern baldness, or subjects who have a wound or who have
CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a CpG oligonucleotide which is used in the exemplification of
CC the present invention.
XX
SQ Sequence 16 BP; 2 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
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Db 1 ACTCTGGAGCGTTCTC 16

RESULT 2
AAH68311/c
ID AAH68311 standard; DNA; 1125 BP.
XX
AC AAH68311;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 3346.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
DR P-PSDB; AAG93092.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 3346; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 1125 BP; 273 A; 355 C; 283 G; 214 T; 0 U; 0 Other;

Query Match 93.8%; Score 15; DB 5; Length 1125;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
|||||||||||||||
Db 372 CTCTGGAGCGTTCTC 358

RESULT 3
ABK85615/c
ID ABK85615 standard; DNA; 1230 BP.
XX
AC ABK85615;
XX
DT 16-AUG-2002 (first entry)
XX
DE DNA encoding murine NET protein.
XX
KW NET; mouse; gene; ds; ERP; SAP-1; angiogenesis; transgenic; ulcer;
KW ischaemia; wound healing; vascular restenosis; hypertension; dementia;
KW alzheimer's disease; lymphoedema; atherosclerosis; haemangioma; bone;
KW haemangioendothelioma; ovarian hyperstimulation; endometriosis; ascites;
KW follicular cyst; Kaposi sarcoma; tumour; cancer; allergy; synovitis;
KW respiratory distress; rheumatoid arthritis; pneumonia; thyroiditis;
KW cartilage dysfunction; obesity; asthma; inflammation; hepatitis;
KW glomerulonephritis; diabetic retinopathy; thyroiditis; nasal polyp;
KW chromosome 10C-D1.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1. .1230
FT /*tag= a
FT /product= "Mouse NET protein"
XX
PN EP1202065-A1.
XX
PD 02-MAY-2002.
XX
PF 25-OCT-2000; 2000EP-00402968.
XX
PR 25-OCT-2000; 2000EP-00402968.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Wasylyk B, Multon M, Ayadi A, Zheng H;
XX
DR WPI; 2002-437317/47.
DR P-PSDB; AAU97931.
XX
PT Use of all or part of a NET polypeptide to identify compounds useful to
PT modulate angiogenesis and prevent or treat pathologies associated with
PT angiogenic disorders e.g. cardiac ischemia, atherosclerosis or tumor
PT growth.
XX
PS Disclosure; Page 36-39; 77pp; English.
XX
CC This invention relates to the use of all or part of a NET (also known as
CC ERP or SAP-1) polypeptide to identify compounds modulating angiogenesis
CC or compounds that can be used to prevent or treat pathologies associated

CC with angiogenic disorders. The invention also comprises transgenic
CC animals that bear mutations in the NET gene. The method and transgenic
CC animals of the invention are useful to identify compounds to treat
CC pathologies associated with angiogenic disorders involving insufficient
CC vascularisation and requiring increased angiogenesis (e.g. cardiac/
CC peripheral ischaemia, defects in wound healing and vascular restenosis,
CC hypertension, ulcers, alzheimer's disease, lymphooedema, dementia) or
CC involving increased vascularisation and requiring decreased angiogenesis
CC (e.g. atherosclerosis, haemangioma, haemangioendothelioma, ovarian
CC hyperstimulation, endometriosis, ascites, follicular cysts,). They are
CC also useful to identify compounds useful to treat pathologies associated
CC with angiogenic disorders such as Kaposi sarcoma, tumour growth and
CC cancer, or other pathologies in which NET is activated). Such compounds
CC may also be used to treat allergies, dysfunctional uterine bleeding,
CC respiratory distress, rheumatoid arthritis, bone and cartilage
CC dysfunction, obesity, synovitis, inflammation, hepatitis,
CC glomerulonephritis, asthma, retinopathy, thyroiditis, pneumonia, nasal
CC polyps and thyroiditis. Such compounds may be e.g. antisense
CC polynucleotides downregulating or blocking expression of a NET gene,
CC intracellular binding proteins or NET dominant negative mutants.
CC Compounds modulating NET activity may also be included in medicaments to
CC prevent and/or treat pathologies associated with angiogenic disorders.
CC The present sequence represents the DNA encoding the mouse NET protein
CC used in the method of the invention, the gene encoding this protein is
CC located on murine chromosome 10C-D1
XX
SQ Sequence 1230 BP; 278 A; 415 C; 285 G; 252 T; 0 U; 0 Other;

Query Match 93.8%; Score 15; DB 6; Length 1230;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
||||||||||||||||
Db 468 CTCTGGAGCGTTCTC 454

RESULT 4
ADE61030/c
ID ADE61030 standard; DNA; 2979 BP.
XX
AC ADE61030;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human gene AF069072, SEQ ID NO 6944.
XX
KW Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; AF069072.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human DNA (shown in Table 2 of the
CC specification) which encodes one of the polypeptides of the invention
CC which is differentially expressed during pain. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2979 BP; 904 A; 721 C; 735 G; 619 T; 0 U; 0 Other;

Query Match 93.8%; Score 15; DB 10; Length 2979;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
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Db 415 CTCTGGAGCGTTCTC 401

RESULT 5
ADE61034/c
ID ADE61034 standard; DNA; 2979 BP.
XX
AC ADE61034;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human gene AF069072, SEQ ID NO 6948.
XX
KW Human; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;

XX
DR WPI; 2003-268312/26.
DR GENBANK; AF069072.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human DNA (shown in Table 2 of the
CC specification) which encodes one of the polypeptides of the invention
CC which is differentially expressed during pain. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2979 BP; 904 A; 721 C; 735 G; 619 T; 0 U; 0 Other;

Query Match 93.8%; Score 15; DB 10; Length 2979;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
||||||||||||||||
Db 415 CTCTGGAGCGTTCTC 401

RESULT 6
AAH68534
ID AAH68534 standard; DNA; 309400 BP.
XX
AC AAH68534;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7069.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;

Query Match 93.8%; Score 15; DB 5; Length 309400;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
||||||||||||||||
Db 226316 CTCTGGAGCGTTCTC 226330

RESULT 7
AAC80587
ID AAC80587 standard; DNA; 16 BP.
XX
AC AAC80587;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:7.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX

PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 25; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

```
  Query Match             90.0%;  Score 14.4;  DB 4;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16
```

RESULT 8
AAS09557
ID AAS09557 standard; DNA; 16 BP.
XX
AC AAS09557;
XX
DT 26-SEP-2001 (first entry)
XX
DE Immunoreactive CpG sequence-containing oligonucleotide #7.
XX
KW CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
OS Synthetic.
XX
PN WO200151500-A1.
XX
PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001122.
XX
PR 14-JAN-2000; 2000US-0176115P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-442129/47.
XX
PT Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
PS Claim 5; Page 28; 48pp; English.
XX
CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon
CC gamma (IFN-gamma) production or a humoral immune response involving B
CC cell activation, antibody and interleukin-6 production in a host, for
CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
CC cancer, e.g. solid tumour cancer, a disease associated with the immune
CC system e.g. autoimmune disorder or an immune system deficiency, infection
CC or a symptom resulting from exposure to bio-warfare agent in a human. The
CC induction of immune response improves the efficacy of a vaccine and is
CC used in antisense therapy. The ODN are useful for treating, preventing or
CC ameliorating allergic reactions, including eczema, allergic rhinitis or
CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
CC and other atopic conditions, for improving the efficacy of vaccines
CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
CC malaria, for treating immune system deficiencies, e.g. lupus
CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
CC multiple sclerosis, infections including Francisella, schistosomiasis,
CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
CC Anthrax and Listeria
XX
SQ Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

```
  Query Match             90.0%;  Score 14.4;  DB 4;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16
```

RESULT 9
ABL35643
ID ABL35643 standard; DNA; 16 BP.
XX
AC ABL35643;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 569.

```
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .16
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 62; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 10
ABL35670
ID   ABL35670 standard; DNA; 16 BP.
XX
AC   ABL35670;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 596.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .16
FT                   /*tag=  a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 63; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 11
ABL35629
ID   ABL35629 standard; DNA; 16 BP.
XX
AC   ABL35629;
XX
DT   04-APR-2002  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO: 555.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
```

```
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .16
FT                   /*tag= a
FT                   /note= "optionally thymidine is replaced by uracil to
FT                   form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT                   least one other base through a ribose sugar"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 11; Page 62; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 12
ABK46435
ID   ABK46435 standard; DNA; 16 BP.
XX
AC   ABK46435;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Immunostimulatory unmethylated CpG oligodideoxynucleotide #25.
XX
KW   unmethylated CpG; oligdideoxynucleotide; ODN; virucide; vaccine;
KW   Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
KW   viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW   bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS   Synthetic.
XX
PN   WO200211761-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US041633.
XX
PR   10-AUG-2000; 2000US-0224011P.
PR   01-SEP-2000; 2000US-0229307P.
XX
PA   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI   Mond JJ,  Prince G,  Klinman DM;
XX
DR   WPI; 2002-227118/28.
XX
PT   Vaccine for immunizing patient against respiratory syncytial virus, has
PT   epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
PT   linked by phosphate bond-oligodideoxynucleotides.
XX
PS   Claim 4; Page 7; 30pp; English.
XX
CC   The invention describes a vaccine comprising one or more epitopes of a
CC   Paramyxoviridae F protein, and one or more CpG (cytosine followed by
CC   guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
CC   vaccine is useful for vaccinating a patient especially against viruses of
CC   the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
CC   primary cause of viral bronchiolitis and pneumonia in infants and
CC   children, and infectious pulmonary disease in infants. RSV has been
CC   particularly implicated in death of infants that are premature, have
CC   bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC   represents an oligodideoxynucleotide that can be used in the creation of
CC   the vaccine
XX
SQ   Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 13
ACC83067
ID   ACC83067 standard; DNA; 16 BP.
XX
AC   ACC83067;
XX
DT   27-AUG-2003  (first entry)
XX
DE   K class CpG ODN sequence useful for encapsulating in SSCL, K19.
XX
KW   Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW   tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW   thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW   schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW   asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW   CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW   multiple sclerosis; infection; tumour; ss.
XX
OS   Unidentified.
XX
PN   WO2003040308-A2.
XX
PD   15-MAY-2003.
XX
PF   29-JUL-2002; 2002WO-US024235.
XX
PR   27-JUL-2001; 2001US-0308283P.
```

PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10A; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a K class CpG
CC ODN potentially useful for encapsulating in SSCL
XX
SQ Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 90.0%; Score 14.4; DB 9; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
||||| |||||||||||
Db 1 ACTCTCGAGCGTTCTC 16

RESULT 14
ADD01102
ID ADD01102 standard; DNA; 16 BP.
XX
AC ADD01102;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG K oligonucleotide SEQ ID NO:66.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnerary; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
PN WO2003054161-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
PA (UYTE-) UNIV TENNESSEE RES CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Zheng M, Rouse BT;
XX
DR WPI; 2003-559138/52.
XX
PT Inducing the production of vascular endothelial growth factor by a cell,
PT useful for inducing angiogenesis, comprises contacting the cell with a
PT CpG oligodeoxynucleotide.
XX
PS Example 7; SEQ ID NO 66; 37pp; English.
XX
CC The present invention describes a method for inducing the production of
CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
CC the cell with a CpG oligonucleotide and therefore inducing the production
CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
CC tissue, comprising introducing a CpG oligonucleotide into an area of the
CC tissue where the formation of new blood vessels is desired, and so
CC inducing neovascularisation in the area of the tissue; (2) promoting
CC angiogenesis in an area of the subject where angiogenesis is desired,
CC comprising introducing a CpG oligonucleotide to the area, and so
CC promoting angiogenesis in the subject; and (3) screening for an agent
CC that inhibits neovascularisation, comprising administering a CpG
CC oligonucleotide to a non-human mammal and administering the agent to the
CC mammal, where inhibition of angiogenesis in the animal indicates that the
CC agent is effective in inhibiting neovascularisation. The CpG
CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
CC activities, and can be used in gene therapy. The method and the CpG
CC oligonucleotides can be used in inducing angiogenesis or
CC neovascularisation, such as in subjects with a skin graft, subjects who
CC exhibit male pattern baldness, or subjects who have a wound or who have
CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a CpG oligonucleotide which is used in the exemplification of
CC the present invention.
XX
SQ Sequence 16 BP; 2 A; 6 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 90.0%; Score 14.4; DB 10; Length 16;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
||||| |||||||||||
Db 1 ACTCTCGAGCGTTCTC 16

RESULT 15
AAC80594
ID AAC80594 standard; DNA; 17 BP.
XX
AC AAC80594;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:14.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.

XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 26; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targetting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 90.0%; Score 14.4; DB 4; Length 17;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
||||| ||||||||||
Db 2 ACTCTCGAGCGTTCTC 17

Search completed: April 29, 2005, 06:26:06
Job time : 165.135 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:15:22 ; Search time 1500.11 Seconds
(without alignments)
405.990 Million cell updates/sec

Title: US-10-068-160A-73
Perfect score: 16
Sequence: 1 actctggagcgttctc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	264	6	CD081179	CD081179 MA3-9999U
c	2	16	100.0	948	2	BE972956	BE972956 601651808
	3	15	93.8	199	6	CA778499	CA778499 MPL384_9_
	4	15	93.8	412	7	CO323806	CO323806 EK191532.
	5	15	93.8	428	1	AI401438	AI401438 tg64a08.x
c	6	15	93.8	445	8	AQ472178	AQ472178 CITBI-E1-
	7	15	93.8	480	8	AQ526058	AQ526058 HS_5309_B
	8	15	93.8	495	8	AZ141640	AZ141640 SP_0045_A
	9	15	93.8	508	2	AW367384	AW367384 MR0-HT016
	10	15	93.8	521	6	CD205752	CD205752 HS1_18_E0
	11	15	93.8	544	8	AF005835	AF005835 AF005835
c	12	15	93.8	555	2	BE013283	BE013283 123182 MA
c	13	15	93.8	555	4	BI344753	BI344753 373312 MA
c	14	15	93.8	561	4	BI344749	BI344749 373307 MA
	15	15	93.8	640	8	BH501762	BH501762 BOHFO59TF
c	16	15	93.8	654	5	BU106109	BU106109 603005752
c	17	15	93.8	659	5	BX925700	BX925700 BX925700
	18	15	93.8	698	8	BZ805477	BZ805477 PUFHH39TD
c	19	15	93.8	699	8	BZ805475	BZ805475 PUFHH39TB
c	20	15	93.8	703	8	BZ005611	BZ005611 oek65f04.
	21	15	93.8	796	9	CW019280	CW019280 ZMMBLc001
c	22	15	93.8	887	7	CK402485	CK402485 AUF_IfInt
	23	15	93.8	944	5	BQ652192	BQ652192 AGENCOURT
c	24	15	93.8	947	4	BG169117	BG169117 602320566
	25	15	93.8	1031	5	BQ921588	BQ921588 AGENCOURT
c	26	15	93.8	1090	2	BE389805	BE389805 601282995
	27	14.4	90.0	117	5	BQ311300	BQ311300 PM4-BN006
c	28	14.4	90.0	152	8	B81058	B81058 CIT-HSP-206
	29	14.4	90.0	173	1	AT002309	AT002309 AT002309
	30	14.4	90.0	222	5	BU993490	BU993490 HD13L13r
	31	14.4	90.0	265	6	CB884492	CB884492 Ma1072 Ha
c	32	14.4	90.0	287	2	BF561461	BF561461 UI-R-C0-h
	33	14.4	90.0	291	1	AU257096	AU257096 AU257096
	34	14.4	90.0	293	1	AL840593	AL840593 AL840593
c	35	14.4	90.0	304	6	CA748391	CA748391 NS_EST_34
	36	14.4	90.0	321	6	CD345249	CD345249 EtESTef87
	37	14.4	90.0	322	7	D59115	D59115 HUM522B03B
	38	14.4	90.0	338	5	BP944962	BP944962 BP944962
	39	14.4	90.0	345	5	BY106539	BY106539 BY106539
c	40	14.4	90.0	348	7	N22914	N22914 yx66g01.s1
	41	14.4	90.0	361	8	AZ260811	AZ260811 RPCI-23-1
c	42	14.4	90.0	366	5	BQ791558	BQ791558 E3220 Chi
	43	14.4	90.0	376	8	BH362657	BH362657 CH230-48C
c	44	14.4	90.0	380	1	AI478296	AI478296 tm44h09.x
	45	14.4	90.0	380	1	AL841666	AL841666 AL841666

ALIGNMENTS

RESULT 1
CD081179
LOCUS CD081179 264 bp mRNA linear EST 14-SEP-2003
DEFINITION MA3-9999U-M319-D07-U.G MA3-0001 Schistosoma mansoni cDNA clone MA3-9999U-M319-D07.G, mRNA sequence.
ACCESSION CD081179
VERSION CD081179.1 GI:34632171
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 264)
AUTHORS Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
TITLE Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE 22879926
PUBMED 12973350
COMMENT Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP, Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MA3-9999U-M319 row: 7 column: D.
FEATURES Location/Qualifiers
source 1. .264
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MA3-9999U-M319-D07.G"
/sex="mixed pool"

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                     /dev_stage="adult"
                     /lab_host="Mus musculus"
                     /clone_lib="MA3-0001"
ORIGIN

  Query Match             100.0%;  Score 16;  DB 6;  Length 264;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db         35 ACTCTGGAGCGTTCTC 50


RESULT 2
BE972956/c
LOCUS       BE972956                948 bp    mRNA    linear   EST 04-OCT-2000
DEFINITION  601651808R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935448 3',
            mRNA sequence.
ACCESSION   BE972956
VERSION     BE972956.1  GI:10586292
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 948)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM777  row: o  column: 01.
FEATURES             Location/Qualifiers
     source          1. .948
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3935448"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_82"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).   Average insert size
                     1.35 kb (range 0.9-4.0 kb).  14/15 colonies contained
                     inserts by PCR. This library was enriched for full-length
                     clones and was constructed by Clontech  Laboratories (Palo
                     Alto, CA)."
ORIGIN

  Query Match             100.0%;  Score 16;  DB 2;  Length 948;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        711 ACTCTGGAGCGTTCTC 696


RESULT 3
CA778499
LOCUS       CA778499                199 bp    mRNA    linear   EST 03-DEC-2002
DEFINITION  MPL384_9_H02 MPL Sus scrofa cDNA clone pSPORT1 5', mRNA sequence.
ACCESSION   CA778499
VERSION     CA778499.1  GI:26016374
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 199)
  AUTHORS   Center for Animal Functional Genomics.
  TITLE     Generation of ESTs from mixed pig cDNA libraries
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Steven P. Suchyta
            Center for Animal Functional Genomics, Department of Animal Science
            Michigan State University
            B215 Anthony Hall, East Lansing, MI 48824, USA
            Tel: 517 355 8443
            Fax: 517 432 9168
            Email: suchytas@msu.edu
            Single Pass sequencing. Bases called and alt-trimmed with phred
            v0.0204425.c. Vector identified by cross_match with the -minscore
            20 -minmatch 12 options.
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .199
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="pSPORT1"
                     /sex="Male and female"
                     /tissue_type="pooled"
                     /dev_stage="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MPL"
                     /note="Organ: pooled; Vector: pSPORT1; Site_1: NotI;
                     Site_2: SalI; Library made from pooled tissue from
                     adipose, adrenal gland, blood leukocytes, brain,
                     cartilage, eye, heart, intestine, kidney, liver, lung
                     lymph nodes, mammary gland, myogenic satellite cells,
                     ovary, pancreas, pituitary gland, placenta, skin, spinal
                     cord, spleen, stomach, tendon, testes, uterus, and
                     vascular from various developmental and physiological
                     stages."
ORIGIN

  Query Match             93.8%;  Score 15;  DB 6;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCT 15
              |||||||||||||||
Db         69 ACTCTGGAGCGTTCT 83


RESULT 4
CO323806
LOCUS       CO323806                412 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  EK191532.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila
            melanogaster cDNA clone EK191532 5, mRNA sequence.
ACCESSION   CO323806
VERSION     CO323806.1  GI:49382240
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Kopczynski,C., Platt,D., Campbell,J., Muzong,C., Laufer,A.,
            Peterson,E. and Swimmer,C.
  TITLE     Exelixis FlyTag EST Project CK01 Library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Stapleton, M.
            BDGP
```

```
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: EK.1915  row: C  column: 8
            High quality sequence stop: 393.
FEATURES             Location/Qualifiers
     source          1. .412
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="EK191532"
                     /clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
                     /note="Organ: mixed stage embryos, imaginal disks, and
                     adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
                     XhoI; Random primed, normalized library from mixed stage
                     embryos, imaginal disks, and adult heads."
ORIGIN

  Query Match             93.8%;  Score 15;  DB 7;  Length 412;
  Best Local Similarity   93.8%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||||||||||| ||
Db        393 ACTCTGGAGCGTTNTC 408


RESULT 5
AI401438
LOCUS       AI401438                428 bp    mRNA    linear   EST 30-MAR-1999
DEFINITION  tg64a08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2113526
            3', mRNA sequence.
ACCESSION   AI401438
VERSION     AI401438.1  GI:4244525
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1814  Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1. .428
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2113526"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NhHMPu_S1"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
ORIGIN

  Query Match             93.8%;  Score 15;  DB 1;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              |||||||||||||||
Db        338 CTCTGGAGCGTTCTC 352


RESULT 6
AQ472178/c
LOCUS       AQ472178                445 bp    DNA     linear   GSS 23-APR-1999
DEFINITION  CITBI-E1-2589E3.TR CITBI-E1 Homo sapiens genomic clone 2589E3,
            genomic survey sequence.
ACCESSION   AQ472178
VERSION     AQ472178.1  GI:4655832
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 445)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .445
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2589E3"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 8;  Length 445;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              |||||||||||||||
Db        182 CTCTGGAGCGTTCTC 168


RESULT 7
AQ526058
LOCUS       AQ526058                480 bp    DNA     linear   GSS 11-MAY-1999
DEFINITION  HS_5309_B1_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=885 Col=23 Row=B, genomic survey sequence.
ACCESSION   AQ526058
VERSION     AQ526058.1  GI:4773378
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 885  row: B  column: 23
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 480.
FEATURES             Location/Qualifiers
     source          1. .480
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=885 Col=23 Row=B"
                     /sex="male"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 8;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db         68 CTCTGGAGCGTTCTC 82


RESULT 8
AZ141640
LOCUS       AZ141640                495 bp    DNA     linear   GSS 28-AUG-2000
DEFINITION  SP_0045_A1_C04_SP6E Strongylocentrotus purpuratus, purple sea
            urchin, sperm genomic BAC library Strongylocentrotus purpuratus
            genomic clone Plate=45 Col=7 Row=E, genomic survey sequence.
ACCESSION   AZ141640
VERSION     AZ141640.1  GI:8293543
KEYWORDS    GSS.
SOURCE      Strongylocentrotus purpuratus
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
            Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
            Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H.
            and Hood,L.
  TITLE     A sea urchin genome project: Sequence scan, virtual map, and
            additional resources
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
  MEDLINE   20402566
   PUBMED   10920195
COMMENT     Contact: Cameron, RA, Davidson, EH, Hood, L
            Division of Biology 156-29
            California Institute of Technology
            Pasadena California 91125, USA
            Tel: (626) 395-8421
            Fax: (626) 793-3047
            Email: acameron@caltech.edu
            Plate: 45  row: E  column: 7
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .495
                     /organism="Strongylocentrotus purpuratus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7668"
                     /clone="Plate=45 Col=7 Row=E"
                     /clone_lib="Strongylocentrotus purpuratus, purple sea
                     urchin, sperm genomic BAC library"
                     /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                     DH10B"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 8;  Length 495;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        311 CTCTGGAGCGTTCTC 325


RESULT 9
AW367384
LOCUS       AW367384                508 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  MR0-HT0164-191099-002-a04 HT0164 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW367384
VERSION     AW367384.1  GI:6872034
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-HT0164-
            191099-002-a04&t3=1999-10-19&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 8
            High quality sequence stop: 507.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0164"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
```

Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 93.8%; Score 15; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
||||||||||||||||
Db 31 CTCTGGAGCGTTCTC 45

RESULT 10
CD205752
LOCUS CD205752 521 bp mRNA linear EST 20-MAY-2003
DEFINITION HS1_18_E02.b1_A012 Heat-shocked seedlings Sorghum bicolor cDNA clone HS1_18_E02_A012 3', mRNA sequence.
ACCESSION CD205752
VERSION CD205752.1 GI:30936132
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 521)
AUTHORS Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Buchanan,C.D., Eastman,A. and Pratt,L.H.
TITLE An EST database from Sorghum: heat-shocked seedlings
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: HS1_18_E02.g1_A012
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .521
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="IS3620C"
/db_xref="taxon:4558"
/clone="HS1_18_E02_A012"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Heat-shocked seedlings"
/note="Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The library was prepared from polyA+ RNA from 6-day-old seedlings grown in hydroponic culture and heat-shocked at 40-42 C for 4 or 24 hr. After heat shock, roots and leaves were harvested and tissues combined for RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG)."

ORIGIN

Query Match 93.8%; Score 15; DB 6; Length 521;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
||||||||||||||||
Db 335 CTCTGGAGCGTTCTC 349

RESULT 11
AF005835
LOCUS AF005835 544 bp DNA linear GSS 06-NOV-2000
DEFINITION AF005835 Arabidopsis thaliana 332-2 Arabidopsis thaliana genomic clone 3322e1 similar to A. thaliana cyclin 3b mRNA with GenBank Accession Number Z31402, genomic survey sequence.
ACCESSION AF005835
VERSION AF005835.1 GI:3387759
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 544)
AUTHORS Mathur,J., Szabados,L., Schaefer,S., Grunenberg,B., Lossow,A., Jonas-Straube,E., Schell,J., Koncz,C. and Koncz-Kalman,Z.
TITLE Gene identification with sequenced T-DNA tags generated by transformation of Arabidopsis cell suspension
JOURNAL Plant J. 13 (5), 707-716 (1998)
MEDLINE 98345991
PUBMED 9681013
COMMENT Contact: Koncz C
Abteilung Genetische Grundlagen der Pflanzenzuechtung
Max-Planck Institut fuer Zuechtungsforschung
Carl von Linne weg 10, Cologne, D-50829, Germany
Email: koncz@mpiz-koeln.mpg.de
transgenic cell line was obtained by transformation with the T-DNA of pPCV6NFHyg Agrobacterium binary vector; the left border junction of T-DNA insertion 3322e1 was isolated in E. coli after EcoRI digestion and self-circularization of plant DNA; clone 3322e1 carries a plant DNA fragment of 6.4 kb that extends from an EcoRI site to the left-border junction of pPCV6NFHyg T-DNA tag; sequences of the left T-DNA border are excluded from the submission
Class: transposon-tagged.
FEATURES Location/Qualifiers
source 1. .544
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-1"
/db_xref="taxon:3702"
/clone="3322e1"
/cell_line="332-2"
/clone_lib="Arabidopsis thaliana 332-2"

ORIGIN

Query Match 93.8%; Score 15; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGAGCGTTCTC 16
||||||||||||||||
Db 236 CTCTGGAGCGTTCTC 250

RESULT 12
BE013283/c
LOCUS BE013283 555 bp mRNA linear EST 09-JUL-2000
DEFINITION 123182 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE013283
VERSION BE013283.1 GI:8274246
KEYWORDS EST.
SOURCE Sus scrofa (pig)

```
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 50  row: D  column: 17
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 1PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
ORIGIN

  Query Match             93.8%;  Score 15;  DB 2;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        548 CTCTGGAGCGTTCTC 534


RESULT 13
BI344753/c
LOCUS       BI344753                555 bp    mRNA    linear   EST 30-JUL-2001
DEFINITION  373312 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI344753
VERSION     BI344753.1  GI:15038042
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 120  row: L  column: 3
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 2PIG"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
ORIGIN

  Query Match             93.8%;  Score 15;  DB 4;  Length 555;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        409 CTCTGGAGCGTTCTC 395


RESULT 14
BI344749/c
LOCUS       BI344749                561 bp    mRNA    linear   EST 30-JUL-2001
DEFINITION  373307 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI344749
VERSION     BI344749.1  GI:15038038
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
            Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Porcine gene discovery by normalized cDNA-library sequencing and
            EST cluster assembly
  JOURNAL   Mamm. Genome 13 (8), 475-478 (2002)
  MEDLINE   22213789
   PUBMED   12226715
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 120  row: K  column: 4
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 2PIG"
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                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
ORIGIN

  Query Match             93.8%;  Score 15;  DB 4;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        407 CTCTGGAGCGTTCTC 393


RESULT 15
BH501762
LOCUS       BH501762                640 bp    DNA     linear   GSS 13-DEC-2001
DEFINITION  BOHFO59TF BOHF Brassica oleracea genomic clone BOHFO59, genomic
            survey sequence.
ACCESSION   BH501762
VERSION     BH501762.1  GI:17709859
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHFO59TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHFO59"
                     /clone_lib="BOHF"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             93.8%;  Score 15;  DB 8;  Length 640;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        149 CTCTGGAGCGTTCTC 163


Search completed: April 29, 2005, 11:55:30
Job time : 1504.11 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 05:17:55 ; Search time 46.8108 Seconds
(without alignments)
559.282 Million cell updates/sec

Title: US-10-068-160A-73
Perfect score: 16
Sequence: 1 actctggagcgttctc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.4	90.0	20	3	US-08-386-063-8	Sequence 8, Appli
2	14.4	90.0	20	3	US-08-386-063-10	Sequence 10, Appl
3	14.4	90.0	20	3	US-08-386-063-8	Sequence 8, Appli
4	14.4	90.0	20	3	US-08-386-063-10	Sequence 10, Appl
5	14.4	90.0	20	3	US-08-738-652-18	Sequence 18, Appl
6	14.4	90.0	20	3	US-08-738-652-19	Sequence 19, Appl
7	14.4	90.0	20	3	US-08-738-652-20	Sequence 20, Appl
8	14.4	90.0	20	3	US-08-738-652-21	Sequence 21, Appl
9	14.4	90.0	20	3	US-09-286-098-7	Sequence 7, Appli
10	14.4	90.0	20	3	US-09-286-098-8	Sequence 8, Appli
11	14.4	90.0	20	3	US-09-286-098-9	Sequence 9, Appli
12	14.4	90.0	20	3	US-09-286-098-10	Sequence 10, Appl
13	14.4	90.0	20	3	US-09-286-098-37	Sequence 37, Appl
14	14.4	90.0	20	3	US-09-286-098-40	Sequence 40, Appl
15	14.4	90.0	20	3	US-08-960-774-15	Sequence 15, Appl
16	14.4	90.0	20	3	US-08-960-774-17	Sequence 17, Appl
17	14.4	90.0	20	3	US-09-325-193A-7	Sequence 7, Appli
18	14.4	90.0	20	3	US-09-325-193A-8	Sequence 8, Appli
19	14.4	90.0	20	3	US-09-325-193A-9	Sequence 9, Appli
20	14.4	90.0	20	3	US-09-325-193A-31	Sequence 31, Appl
21	14.4	90.0	20	3	US-09-325-193A-33	Sequence 33, Appl
22	14.4	90.0	20	3	US-09-325-193A-34	Sequence 34, Appl
23	14.4	90.0	20	3	US-09-191-170-7	Sequence 7, Appli
24	14.4	90.0	20	3	US-09-191-170-8	Sequence 8, Appli
25	14.4	90.0	20	3	US-09-191-170-9	Sequence 9, Appli
26	14.4	90.0	20	3	US-09-191-170-10	Sequence 10, Appl
27	14.4	90.0	20	3	US-09-191-170-37	Sequence 37, Appl
28	14.4	90.0	20	4	US-09-337-619-15	Sequence 15, Appl
29	14.4	90.0	20	4	US-09-337-619-17	Sequence 17, Appl
30	14.4	90.0	21	3	US-09-286-098-39	Sequence 39, Appl
c 31	14.4	90.0	601	4	US-09-949-016-205840	Sequence 205840,
32	14.4	90.0	1747	4	US-09-244-805-23	Sequence 23, Appl
c 33	14.4	90.0	1997	2	US-08-750-134A-6	Sequence 6, Appli
c 34	14.4	90.0	1997	3	US-09-363-745-6	Sequence 6, Appli
35	14.4	90.0	10917	3	US-08-926-842B-11	Sequence 11, Appl
36	14.4	90.0	62804	3	US-09-800-960-3	Sequence 3, Appli
37	14.4	90.0	62804	4	US-10-096-960-3	Sequence 3, Appli
38	14.4	90.0	69909	4	US-09-949-016-13423	Sequence 13423, A
c 39	14.4	90.0	305491	4	US-09-949-016-17550	Sequence 17550, A
40	14.4	90.0	455726	4	US-09-949-016-14157	Sequence 14157, A
41	14.4	90.0	481115	4	US-09-949-016-11940	Sequence 11940, A
42	14	87.5	20	3	US-08-386-063-9	Sequence 9, Appli
43	14	87.5	20	3	US-08-386-063-9	Sequence 9, Appli
44	14	87.5	20	3	US-08-960-774-16	Sequence 16, Appl
45	14	87.5	20	4	US-09-337-619-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-386-063-8
; Sequence 8, Application US/08386063
; Patent No. 6008200
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,063
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ARNOLD, BETH E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIZ-013CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-386-063-8

Query Match 90.0%; Score 14.4; DB 3; Length 20;
Best Local Similarity 93.8%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20
```

RESULT 2

```
US-08-386-063-10
; Sequence 10, Application US/08386063
; Patent No. 6008200
;  GENERAL INFORMATION:
;    APPLICANT:  Arthur M. Krieg, M.D.
;    TITLE OF INVENTION:  IMMUNOMODULATORY OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/386,063
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ARNOLD, BETH E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  UIZ-013CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  3
;      OTHER INFORMATION:  "N indicates 5 methyl cytosine"
US-08-386-063-10

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 3
US-08-386-063-8
; Sequence 8, Application US/08386063
; Patent No. 6194388
;  GENERAL INFORMATION:
;    APPLICANT:  Arthur M. Krieg, M.D.
;    TITLE OF INVENTION:  IMMUNOMODULATORY OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/386,063
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ARNOLD, BETH E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  UIZ-013CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-386-063-8

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 4
US-08-386-063-10
; Sequence 10, Application US/08386063
; Patent No. 6194388
;  GENERAL INFORMATION:
;    APPLICANT:  Arthur M. Krieg, M.D.
;    TITLE OF INVENTION:  IMMUNOMODULATORY OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/386,063
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ARNOLD, BETH E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  UIZ-013CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  3
;      OTHER INFORMATION:  "N indicates 5 methyl cytosine"
US-08-386-063-10

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
```

```
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 5
US-08-738-652-18
; Sequence 18, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
;  FILE REFERENCE: C1039/7004 HCL
;  CURRENT APPLICATION NUMBER: US/08/738,652B
;  CURRENT FILING DATE: 1996-10-30
;  EARLIER APPLICATION NUMBER: US 08/276,358
;  EARLIER FILING DATE: 1994-07-15
;  EARLIER APPLICATION NUMBER: US 08/386,063
;  EARLIER FILING DATE: 1995-02-07
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-18

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 6
US-08-738-652-19
; Sequence 19, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
;  FILE REFERENCE: C1039/7004 HCL
;  CURRENT APPLICATION NUMBER: US/08/738,652B
;  CURRENT FILING DATE: 1996-10-30
;  EARLIER APPLICATION NUMBER: US 08/276,358
;  EARLIER FILING DATE: 1994-07-15
;  EARLIER APPLICATION NUMBER: US 08/386,063
;  EARLIER FILING DATE: 1995-02-07
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (3)...(3)
;   OTHER INFORMATION: m5c
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (10)...(10)
;   OTHER INFORMATION: m5c
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (14)...(14)
;   OTHER INFORMATION: m5c
US-08-738-652-19

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 7
US-08-738-652-20
; Sequence 20, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
;  FILE REFERENCE: C1039/7004 HCL
;  CURRENT APPLICATION NUMBER: US/08/738,652B
;  CURRENT FILING DATE: 1996-10-30
;  EARLIER APPLICATION NUMBER: US 08/276,358
;  EARLIER FILING DATE: 1994-07-15
;  EARLIER APPLICATION NUMBER: US 08/386,063
;  EARLIER FILING DATE: 1995-02-07
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (3)...(3)
;   OTHER INFORMATION: m5c
US-08-738-652-20

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 8
US-08-738-652-21
; Sequence 21, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
;  FILE REFERENCE: C1039/7004 HCL
;  CURRENT APPLICATION NUMBER: US/08/738,652B
;  CURRENT FILING DATE: 1996-10-30
;  EARLIER APPLICATION NUMBER: US 08/276,358
;  EARLIER FILING DATE: 1994-07-15
;  EARLIER APPLICATION NUMBER: US 08/386,063
;  EARLIER FILING DATE: 1995-02-07
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   FEATURE:
```

```
;   NAME/KEY: modified_base
;   LOCATION: (18)...(18)
;   OTHER INFORMATION: m5c
US-08-738-652-21

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 9
US-09-286-098-7
; Sequence 7, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Weiner, George
;  TITLE OF INVENTION: Methods and Products for Stimulating the
;  TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
;  TITLE OF INVENTION: Cytokines
;  FILE REFERENCE: C1039/7026/HCL
;  CURRENT APPLICATION NUMBER: US/09/286,098
;  CURRENT FILING DATE: 1999-04-02
;  EARLIER APPLICATION NUMBER: US 60/080,729
;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: SArtificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-286-098-7

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 10
US-09-286-098-8
; Sequence 8, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Weiner, George
;  TITLE OF INVENTION: Methods and Products for Stimulating the
;  TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
;  TITLE OF INVENTION: Cytokines
;  FILE REFERENCE: C1039/7026/HCL
;  CURRENT APPLICATION NUMBER: US/09/286,098
;  CURRENT FILING DATE: 1999-04-02
;  EARLIER APPLICATION NUMBER: US 60/080,729
;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (3)...(3)
;   OTHER INFORMATION: m5c
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (10)...(10)
;   OTHER INFORMATION: m5c
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (14)...(14)
;   OTHER INFORMATION: m5c
US-09-286-098-8

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 11
US-09-286-098-9
; Sequence 9, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Weiner, George
;  TITLE OF INVENTION: Methods and Products for Stimulating the
;  TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
;  TITLE OF INVENTION: Cytokines
;  FILE REFERENCE: C1039/7026/HCL
;  CURRENT APPLICATION NUMBER: US/09/286,098
;  CURRENT FILING DATE: 1999-04-02
;  EARLIER APPLICATION NUMBER: US 60/080,729
;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (3)...(3)
;   OTHER INFORMATION: m5c
US-09-286-098-9

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 12
US-09-286-098-10
; Sequence 10, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Weiner, George
;  TITLE OF INVENTION: Methods and Products for Stimulating the
;  TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
;  TITLE OF INVENTION: Cytokines
;  FILE REFERENCE: C1039/7026/HCL
;  CURRENT APPLICATION NUMBER: US/09/286,098
;  CURRENT FILING DATE: 1999-04-02
;  EARLIER APPLICATION NUMBER: US 60/080,729
```

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;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (18)...(18)
;   OTHER INFORMATION: m5c
US-09-286-098-10

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 13
US-09-286-098-37
; Sequence 37, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Weiner, George
;  TITLE OF INVENTION: Methods and Products for Stimulating the
;  TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
;  TITLE OF INVENTION: Cytokines
;  FILE REFERENCE: C1039/7026/HCL
;  CURRENT APPLICATION NUMBER: US/09/286,098
;  CURRENT FILING DATE: 1999-04-02
;  EARLIER APPLICATION NUMBER: US 60/080,729
;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-286-098-37

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 14
US-09-286-098-40
; Sequence 40, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Weiner, George
;  TITLE OF INVENTION: Methods and Products for Stimulating the
;  TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
;  TITLE OF INVENTION: Cytokines
;  FILE REFERENCE: C1039/7026/HCL
;  CURRENT APPLICATION NUMBER: US/09/286,098
;  CURRENT FILING DATE: 1999-04-02
;  EARLIER APPLICATION NUMBER: US 60/080,729
;  EARLIER FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (14)...(14)
;   OTHER INFORMATION: m5c
US-09-286-098-40

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          5 ACTCTCGAGCGTTCTC 20


RESULT 15
US-08-960-774-15
; Sequence 15, Application US/08960774
; Patent No. 6239116
;  GENERAL INFORMATION:
;    APPLICANT:  Krieg et al.,
;    TITLE OF INVENTION:  IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/960,774
;      FILING DATE:  30-October-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. Serial No. 6239116  08/738,652
;      FILING DATE:  October 30, 1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  08918/012001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-960-774-15

  Query Match             90.0%;  Score 14.4;  DB 3;  Length 20;
  Best Local Similarity   93.8%;  Pred. No. 78;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
```

Db 5 ACTCTCGAGCGTTCTC 20

Search completed: April 29, 2005, 12:03:07
Job time : 48.9358 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 29, 2005, 06:00:59 ; Search time 214.595 Seconds
(without alignments)
453.893 Million cell updates/sec

Title: US-10-068-160A-73
Perfect score: 16
Sequence: 1 actctggagcgttctc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	100.0	16	14	US-10-068-160-73	Sequence 73, Appl
2	16	100.0	16	15	US-10-194-035-113	Sequence 113, App
3	16	100.0	16	19	US-10-499-597-55	Sequence 55, Appl
4	15	93.8	521	18	US-10-767-701-24463	Sequence 24463, A
5	15	93.8	570	18	US-10-425-115-5311	Sequence 5311, Ap
c 6	15	93.8	1125	9	US-09-738-626-3346	Sequence 3346, Ap
c 7	15	93.8	1230	17	US-10-415-181-3	Sequence 3, Appli
8	15	93.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
9	14.4	90.0	16	11	US-09-874-991C-555	Sequence 555, App
10	14.4	90.0	16	11	US-09-874-991C-569	Sequence 569, App
11	14.4	90.0	16	11	US-09-874-991C-596	Sequence 596, App
12	14.4	90.0	16	14	US-10-068-160-9	Sequence 9, Appli
13	14.4	90.0	16	15	US-10-194-035-7	Sequence 7, Appli
14	14.4	90.0	16	19	US-10-499-597-66	Sequence 66, Appl
15	14.4	90.0	17	15	US-10-194-035-14	Sequence 14, Appl
16	14.4	90.0	18	10	US-09-888-326-188	Sequence 188, App
17	14.4	90.0	18	10	US-09-776-479-724	Sequence 724, App
18	14.4	90.0	18	11	US-09-776-479-724	Sequence 724, App
19	14.4	90.0	18	14	US-10-112-653-697	Sequence 697, App
20	14.4	90.0	18	14	US-10-017-995-724	Sequence 724, App
21	14.4	90.0	18	15	US-10-194-035-11	Sequence 11, Appl
22	14.4	90.0	18	17	US-10-314-578-724	Sequence 724, App
23	14.4	90.0	18	18	US-10-831-778-724	Sequence 724, App
24	14.4	90.0	19	11	US-09-874-991C-554	Sequence 554, App
25	14.4	90.0	19	11	US-09-874-991C-568	Sequence 568, App
26	14.4	90.0	19	11	US-09-874-991C-595	Sequence 595, App
27	14.4	90.0	19	14	US-10-068-160-8	Sequence 8, Appli
28	14.4	90.0	19	15	US-10-194-035-5	Sequence 5, Appli
29	14.4	90.0	19	19	US-10-499-597-59	Sequence 59, Appl
30	14.4	90.0	20	9	US-09-824-468-7	Sequence 7, Appli
31	14.4	90.0	20	9	US-09-824-468-8	Sequence 8, Appli
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33	14.4	90.0	20	9	US-09-824-468-10	Sequence 10, Appl
34	14.4	90.0	20	9	US-09-824-468-37	Sequence 37, Appl
35	14.4	90.0	20	9	US-09-824-468-40	Sequence 40, Appl
36	14.4	90.0	20	9	US-09-800-266A-7	Sequence 7, Appli
37	14.4	90.0	20	9	US-09-800-266A-8	Sequence 8, Appli
38	14.4	90.0	20	9	US-09-800-266A-9	Sequence 9, Appli
39	14.4	90.0	20	9	US-09-800-266A-31	Sequence 31, Appl
40	14.4	90.0	20	9	US-09-800-266A-33	Sequence 33, Appl
41	14.4	90.0	20	9	US-09-800-266A-34	Sequence 34, Appl
42	14.4	90.0	20	9	US-09-846-091-5	Sequence 5, Appli
43	14.4	90.0	20	9	US-09-895-007A-7	Sequence 7, Appli
44	14.4	90.0	20	9	US-09-895-007A-8	Sequence 8, Appli
45	14.4	90.0	20	9	US-09-895-007A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-068-160-73
; Sequence 73, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-73

Query Match 100.0%; Score 16; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
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Db 1 ACTCTGGAGCGTTCTC 16

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RESULT 2
US-10-194-035-113
; Sequence 113, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-113

  Query Match             100.0%;  Score 16;  DB 15;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db          1 ACTCTGGAGCGTTCTC 16


RESULT 3
US-10-499-597-55
; Sequence 55, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Rouse, Barry T.
;  APPLICANT:  Zheng, Mei
;  TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
;  FILE REFERENCE: 4239-64125-02
;  CURRENT APPLICATION NUMBER: US/10/499,597
;  CURRENT FILING DATE:  2004-06-17
;  PRIOR APPLICATION NUMBER: PCT/US02/40955
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,457
;  PRIOR FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CpG K oligonucleotide
US-10-499-597-55

  Query Match             100.0%;  Score 16;  DB 19;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
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Db          1 ACTCTGGAGCGTTCTC 16


RESULT 4
US-10-767-701-24463
; Sequence 24463, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 24463
;   LENGTH: 521
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 30936132
US-10-767-701-24463

  Query Match             93.8%;  Score 15;  DB 18;  Length 521;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
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Db        335 CTCTGGAGCGTTCTC 349


RESULT 5
US-10-425-115-5311
; Sequence 5311, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 5311
;   LENGTH: 570
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_104839C.1
US-10-425-115-5311

  Query Match             93.8%;  Score 15;  DB 18;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
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Db        345 CTCTGGAGCGTTCTC 359


RESULT 6
US-09-738-626-3346/c
; Sequence 3346, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
```

```
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3346
;   LENGTH: 1125
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-3346

  Query Match             93.8%;  Score 15;  DB 9;  Length 1125;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        372 CTCTGGAGCGTTCTC 358


RESULT 7
US-10-415-181-3/c
; Sequence 3, Application US/10415181
; Publication No. US20040053833A1
; GENERAL INFORMATION:
;  APPLICANT: WASYLYK, Bohdan
;  APPLICANT:  MULTON, Marie-Christine
;  APPLICANT:  AYADI, Abdelkader
;  APPLICANT:  ZHENG, Hong
;  TITLE OF INVENTION: NET, A TRANSCRIPTION FACTOR OF THE TCF FAMILY, AS REGULATOR OF
;  TITLE OF INVENTION:  ANGIOGENIC FACTOR EXPRESSION
;  FILE REFERENCE: ST00030 USPCT
;  CURRENT APPLICATION NUMBER: US/10/415,181
;  CURRENT FILING DATE:  2003-04-25
;  PRIOR APPLICATION NUMBER: EP00402968.2
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: PCT/EP01/12987
;  PRIOR FILING DATE: 2001-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 1230
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-415-181-3

  Query Match             93.8%;  Score 15;  DB 17;  Length 1230;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
              ||||||||||||||||
Db        468 CTCTGGAGCGTTCTC 454


RESULT 8
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
;  APPLICANT: NAKAGAWA, SATOSHI
;  APPLICANT:  MIZOGUCHI, HIROSHI
;  APPLICANT:  ANDO, SEIKO
;  APPLICANT:  HAYASHI, MIKIRO
;  APPLICANT:  OCHIAI, KEIKO
;  APPLICANT:  YOKOI, HARUHIKO
;  APPLICANT:  TATEISHI, NAOKO
;  APPLICANT:  SENOH, AKIHIRO
;  APPLICANT:  IKEDA, MASATO
;  APPLICANT:  OZAKI, AKIO
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-125
;  CURRENT APPLICATION NUMBER: US/09/738,626
;  CURRENT FILING DATE:  2000-12-18
;  PRIOR APPLICATION NUMBER: JP 99/377484
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: JP 00/159162
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: JP 00/280988
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 7059
;  SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
;   LENGTH: 3309400
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

  Query Match             93.8%;  Score 15;  DB 9;  Length 3309400;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGAGCGTTCTC 16
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Db    3226316 CTCTGGAGCGTTCTC 3226330


RESULT 9
US-09-874-991C-555
; Sequence 555, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-555

  Query Match             90.0%;  Score 14.4;  DB 11;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
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Db          1 ACTCTCGAGCGTTCTC 16


RESULT 10
US-09-874-991C-569
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; Sequence 569, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 569
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-569

  Query Match             90.0%;  Score 14.4;  DB 11;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 11
US-09-874-991C-596
; Sequence 596, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
;  APPLICANT: MOND, JAMES J.
;  APPLICANT:  FLORA, MICHAEL
;  APPLICANT:  KLINMAN, DENNIS M.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
;  FILE REFERENCE: 07787.0042-0
;  CURRENT APPLICATION NUMBER: US/09/874,991C
;  CURRENT FILING DATE:  2001-06-07
;  PRIOR APPLICATION NUMBER: 60/209,797
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 620
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 596
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-596

  Query Match             90.0%;  Score 14.4;  DB 11;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 12
US-10-068-160-9
; Sequence 9, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
;  APPLICANT:  SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-61999
;  CURRENT APPLICATION NUMBER: US/10/068,160
;  CURRENT FILING DATE:  2002-02-06
;  PRIOR APPLICATION NUMBER: 60/128,898
;  PRIOR FILING DATE: 1999-04-12
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-10-068-160-9

  Query Match             90.0%;  Score 14.4;  DB 14;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 13
US-10-194-035-7
; Sequence 7, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  KLINMAN, Dennis
;  APPLICANT:  ISHII, Ken
;  APPLICANT:  VERTHELYI, Daniela
;  TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
;  FILE REFERENCE: 4239-63317
;  CURRENT APPLICATION NUMBER: US/10/194,035
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: PCT/US01/01122
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/176,115
;  PRIOR FILING DATE: 2000-01-14
;  NUMBER OF SEQ ID NOS: 119
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 16
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-7

  Query Match             90.0%;  Score 14.4;  DB 15;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ACTCTGGAGCGTTCTC 16
              ||||| ||||||||||
Db          1 ACTCTCGAGCGTTCTC 16


RESULT 14
US-10-499-597-66
; Sequence 66, Application US/10499597
; Publication No. US20050026245A1
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
;  APPLICANT:  SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
;  APPLICANT:  Klinman, Dennis M.
;  APPLICANT:  Rouse, Barry T.
;  APPLICANT:  Zheng, Mei
```

; TITLE OF INVENTION: USE OF CPG OLIGODEOXYNUCLEOTIDES TO INDUCE ANGIOGENESIS
; FILE REFERENCE: 4239-64125-02
; CURRENT APPLICATION NUMBER: US/10/499,597
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: PCT/US02/40955
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/343,457
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG K oligonucleotide
US-10-499-597-66

Query Match 90.0%; Score 14.4; DB 19; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
||||| |||||||||||
Db 1 ACTCTCGAGCGTTCTC 16

RESULT 15
US-10-194-035-14
; Sequence 14, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-14

Query Match 90.0%; Score 14.4; DB 15; Length 17;
Best Local Similarity 93.8%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACTCTGGAGCGTTCTC 16
||||| |||||||||||
Db 2 ACTCTCGAGCGTTCTC 17

Search completed: April 29, 2005, 12:35:52
Job time : 219.595 secs